Access DB# 48760.

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:		i	:xaminer # :	Date:		
Requester's Full Name: Art Unit	Phone Number 30	 - '	Serial Number:			
Mail Box and Bldg:Room	Location:	Result	s Format Preferred ic	rcle): PAPEF	DISK	E-MA
more than one search	is submitted, pleas	se prioritize	searches in order o	of need. ******	*****	*****
lease provide a detailed statem include the elected species or st tility of the invention. Define mown Please attach a copy of	ent of the search topic. nictures, keywords, syn any terms that may have	and describe as onyms, acronyi e a special meai	specifically as possible thems, and registry numbers, ning. Give examples or to	ne subject matte and combine w	ith the co	ncept or
Fitle of Invention:						
nventors (please provide full						
Earliest Priority Filing Da						
For Sequence Searches Only F appropriate serial number.	lease include all pertinen	t information (p	arent, child, divisional, or is	sued patent num	bers) along	g with the
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OM protein -
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                                              July 15,
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2003, 06:52:29; Search time 13.4523 Seconds (without alignments) 1657.949 Million cell updates/sec
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Title: Perfect score: Sequence: US-09-847-208B-3

EPKSCDKTHTCPPCPAPELL...........MHEALHNHYQQRSLSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283224

283224 seqs, 96134422 residues

Maximum Minimum DB DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir1:*
pir2:*
pir3:*
pir4:*

Database

PIR_73:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	5	4	ω	2	1	Result No.
776	776	776.5	784.5	784.5	58	94.	801.5	11.	811.5	812.5	813	820	840.5	847.5	858	865	868.5	868.5	883	1097	1107	1123	1136	1138	1172	1217	1219	1225	Score
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	G2MSA	S00847		PS0017	G1MS	PC4436			C30554								147159				G2HU	G3HUWI	A60764	A23511	PT0207	S31866	S69339	GHHU	ID
gamma-2a	gamma-2a		gamma-1 chain	Ig gamma-1 chain C	gamma-1 chain	Ď	gamma-3 chain		heavy ch	gamma-	gamma-2b chai		gamma 3		gamma-2 chain	gamma 4 c	gamma 2a	gamma	gamma chain C	gamma-4 chain	gamma-2	gamma-3 heavy	gamma-3 chain	gamma-3 chain	gamma chain	gamma-1 chain	heavy chain V	Ig gamma-1 chain C	Description

A: Molecule type: DNA
A: Molecule type: DNA
A: Residues: 88-113:235-330 <TAK>
A: Residues: 88-113:235-330 <TAK>
A: Cross-references: EMBL:Z17370
R: Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
Blochemistry 9, 3161-3170, 1970
A: Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A: Reference number: A90563; MUID:71064024; PMID:5489771
A; Contents: myeloma protein Eu
A: Accession: B90563
A: Wolecule type: protein
A: Residues: 1-96, 'R', 98-135 <CUND
A: Residues: 1-96, 'R', 98-135 <R', 98-1

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
353	353	357	366.5	542	547	549	669	731.5	735	746.5	747.5	751.5	761	771	772
28.0	28.0	28.3	29.1	43.0	43.4	43.6	53.1	58.1	58.3	59.2	59.3	59.6	60.4	61.2	61.3
455	343	549	572	152	218	249	180	475	327	405	322	474	446	399	335
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Ig mu chain C regi	Ig mu chain C regi	Ig heavy chain pre	Ig Y heavy chain (Ig gamma-1 chain C	Ig heavy chain V-I	Ig heavy chain VHI	Ig gamma heavy cha	Ig gamma-2b chain	· Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain

ALIGNMENTS

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igen Primaerstruktur
A; Reference number: I
A; Contents: myeloma I
A; Accession: B91668
               Ig heavy chain V region precursor - hun (Speciles: Homo sapiens (man) C:Date: 19-Mar-11997 #sequence_revision C:Accession: S69339; 572664 R:Khamlichi, A.A.; Aucouturier, P.; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;24-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109/112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Complex: An immunoglobulin heterotetramer subunit consists of two ide hain disulfide bonds. In some cases, such as IgA and IgM, the subunits C:Superfamily: immunoglobulin C region; immunoglobulin homology C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin E:20-85/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglo A;Reference number: A90565, MUD:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L; Schwarz, J; Reichel, W; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUD:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
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A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L'
A;Residues: this sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monokionalen Immunglol
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
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A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
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  Aucouturier, P.;
29, 54-60, 1995
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97.08;
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Pred. No. 3.9e-86;
                   Preud'homme,
                                                                                                      human
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PMID:4923144
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                 J.L.;
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C; Date: 06-Jan-1995 #sequer
C; Accession: S31866
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S31866
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A; Residues: 1-255 <FIL>
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A; Accession: S31866
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A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C
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A; Residues: 1-140, 'C', 142-374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data A; Reference number: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
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A; Residues: 1-374 <KHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
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                                                                                                                                                                                                                                                                                                                      Similarity
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                    NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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                                                                                            ISKAKVQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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96.1%;
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                                                                                                                                                                                                                                                                                                                      Score 1219;
Pred. No. 1
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Ig gamma-1 chain C region - C; Species: synthetic synthetic

#sequence_revision 17-Mar-1997 #text_ #text_change 19-May-2000

submitted to the EMBL Data

A; Description: Screeing ata Library, February 1993 method for protein-protein interactions of cloned gene

A; Cross-references: EMBL: x70421; NID: g33068; PIDN: CAA49866.1; PID:g33069

C;Keywords: immunoglobulin F;1-22/Region: Escherichia coli outer membrane F;23-255/Region: human Ig gamma-1 chain C regio chain C region protein Þ precursor

Similarity Conservative 96.6%; Score 1217; DB 4; Pred. No. 1.1e-85; Length Indels 0; Gaps

0;

NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT ESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 120 83 143

ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180 203

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C; Accession: A23511
C; Accession: A23511
R; Huck, S.; Fort, P.; Crawford, D.H.; Lerrano, Nucleic Acids Res. 14, 1779-1789, 1986
A; Title: Sequence of a human immunoglobulin gar A; Reference number: A23511; MUID:86148507; PMT
A; Accession: A23511
A; Accession: A23511
A; Molecule type: DNA
A; Residues: 1-377 CHUC>
A: Cross-references: GB: X03604; GB: M12958; NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Nucleotide sequence of chimpanzee A;Reference number: pT0207; MUID:91287716; A;Accession: pT0207
A;Molecule type: mRNA A;Residues: 1-234 cEHR> C;Superfamily: immunoglobulin C region; imm C;Keywords: immunoglobulin homology <1
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PT0207
PT0207
PT0207
E; Species: Pan troglodytes (chimpanzee)
C; Date: 23-Nov-1991 #sequence_revision:
C; Accession: PT0207
C;
                                                                                                                                                                                                   A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147
A;Cross-references: GDB:119339; OMIM:147
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 16
C;Superfamily: immunoglobulin C region; C;Keywords: immunoglobulin homology
F;20-85/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вp
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       PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
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Pred. No. 2.8e-82;
                                                                                                     Pred. No. 2e-
l; Mismatches
                                                                                                                                                   Score
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PMID:2062315
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PMID:3081877
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A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 A;Note: the sequence of residues 42-76 was taken from the reference that follows R;Michaelsen, T.E.; Franglone, B.; Franklin, E.C.

J. Blol. Chem. 252, 883-889, 1977
A;Title: Primary structure.
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G3HUWI
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A; Residues: 1-377 <HUC>
C; Superfamily: immunoglobulin C
C; Keywords: immunoglobulin F; 20-85/Domain: immunoglobulin h
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                                                                                                                                                                                                Biochemistry 19, 4304-4308, 1980
A;Title: Prinary structure of human gamma3
A;Reference number: A90442; MUID:81021548;
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
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Ig gamma-3 heavy chain useco.
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change
C;Accession: A90442; A92219; A90198; A93915; A02149
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, A90442; A908, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A;Reference number: A60764; MUID:90007613; PMID:2571587 A;Accession: A60764
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Homo sapiens (man)
C; Date: 14-May-1993 #sequence_revision
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Pred. No. 2.8e-79;
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immunoglobulin deletion PMID:6774747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with
                                                                                                                                                                                                                                                                                         377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377
                      mutant: gamma3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265
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Ig gamma-2 chain C region - human
(;Species: Homo saplens (man)
(;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change
(;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobul
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin C:Keywords: duplication; glycoprotein; immunoglobulin; F:203-270/Domain: immunoglobulin homology <IMM>F:1/Modified site: pyrrolidone carboxylic acid (Gln) #sfF;6,140/Binding site: carbohydrate (Asn) (covalent) #st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 59-125, 'EB',128-226,228-289 <WOL>
A; Residues: 59-125, 'EB',128-226,228-289 <WOL>
A; Note: this protein lacks most of the V region, all of the CH1 region, and part of the R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L., Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy Chain disease in man: cDNA sequence supports partial gene deletion A; Reference number: A93915, MUID:82247835; PMID:6808505
A; Contents: heavy chain disease protein Omm
A; Accession: A93915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154;'D',156-15'
A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
C; Comment: The heavy chain disease protein Wis is shown.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A; Title: The amino acid sequence of "heavy chain disease" protein ZUC.
A; Reference number: A90198; MUID: 77021516; PMID: 823945
A; Contents: heavy chain disease protein Zuc, partial sequence correspondence.
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A; Note: cysteines at positions 24, 27, 33, 33, 37, 42

R; Wolfenstein-Todel, C.; Frangione, B.; Prelli, F

R; Wolfenstein-Todel, C.; F

R; Wolfenstein-Todel, C
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A; Map position: 14q32.33-14q32.33
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A;Contents: normal gamma-3 chains, sequence correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A90198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.1%;
88.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1123; DB 1;
No. 2e-78;
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                                                                                                                                                                        immunoglobulin
PIDN:CAB58438.1; PID:g6066056
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A; Residues: 238-275 <HOF>
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Immunol. 16, 923-925,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Contents: myeloma protein Zie
A;Accession: A90752
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              number: A9459
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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   ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               87.9%;
88.4%;
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A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14932.33-14932.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associated by the subunits associated
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A;Residues: 1-19, (°, 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <
A;Residues: 1-19, (°, 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <
A;Rote: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. BioChem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chair
A;Reference number: A90752; MUID:80001357; PMID:113060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,140-200,246-304/Disulfide bonds: #status experimental F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Biochem. J. 121, 217-225, 1971
A;Title: Dissulphide bridges of the heavy chain of human A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Reference number: Myeloma protein Sa, disulfide bo R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
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J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy cha;Reference number: A92809; MUID:81007873; PMID:6774012 A;Contents: myeloma protein Til
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IM1>
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A; Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 1
                                                                                                                                                      NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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PMID:118920
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A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IqA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IM1>
F;30-85/Domain: immunoglobulin homology <IM2>
F;134-203/Domain: immunoglobulin homology <IM2>
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GHRB
Ig gamma chain C region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984
C;Accession: A91749; A90290; A93928; A90245; A94416
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F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;142/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;26-105/Disulfide bonds: interchain (to heavy chain) #status experimental
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MUID:83157104; PMID:6299662
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Biochem. J. 151, 337-349, 197
A;Title: Sequence studies on
A;Reference number: A90290; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A90290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: this sequence has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-323 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Bernstein,
                                                                                                δÃ
                                                                                                                                         В
    RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                      SLSLSPGK
                                                               SISRSPGK
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A;Molecule type: protein
A;Residues: 132-143/E',145-161 <FRU>
A;Residues: 132-143/E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wikse
A;Reference number: A94416
A;Rocession: A94416
A;Molecule type: protein
A;Rocession: A94416
A;Molecule type: protein
A;Rocession: A94416
A;Molecule type: protein
A;Rocession: A954416
A;Molecule type: protein
A;Molec
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A; Residues: 88-103; M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Residues: 88-103; M', 105-26; NID: 9165111; PIDN: AAA31289.1; PID: 9165
A; Note: this sequence has the dl1 allotypic marker, 104-Met, and the
R; Fruchter, R.G., Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A; Title: Sequence studies of the Fd section of the heavy chain of ral
A; Reference number: A90245; MUID: 70110015; PMID: 5461106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Kn
Proc. Natl. Acad. Scl. U.S.A. 79, 6018-6022, 1982
A; Title: Heavy chain genes of rabbit Igg; isolation of a
A; Reference number: A93928; MUID:83299917; PMID:6193512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;130-199/Domain: immunoglobulin homology <IM2> F;236-303/Domain: immunoglobulin homology <IM3> F;173/Binding site: carbohydrate (Asn) (covalen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 < PRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a rabbit IgG heavy chain nce number: A91749; MUID:84030930; PMID:6313520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.E.; Alexander, C.B.; cs 18, 387-397, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVF1FPPKPKDTLM1SRTPEV
                                                                                                                                                                                                                                                                                                                                                                                     TCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEY 104
                                                                                                                                                                                            KCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                                                                                                                                                                                                                                                                                                             TCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPITHQDWLRGKEF
EWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQK
                                        EWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQR
                                                                                                                                                        KCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (covalent) #status
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No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
.5e-60;
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C;Superfamily: immunoglobulin C region; immunoglobulin
F;133-202/Domain: immunoglobulin homology <IMM>
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C;Superfamily: imr
F;133-202/Domain:
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 Qy
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                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-328 < KA
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R; Kacskovics, I.; Su
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A; Residues: 1-328 <KAC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: U03780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Kacskovics,
                                                                                                                                                                                                                                                                    Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                 g gamma 2a chain constant region - pig (fragment); Species: Sus scrofa domestica (domestic pig); Spate: 21-Feb-1997 #sequence_revision 21-Feb-1997
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                                                                                                                                                    Matches
                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                       Kacskovics, I.; Sun, J.; Butler, J.E. Immunol. 153, 3565-3573, 1994
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   131
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                                                                                                       11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                    157;
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                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQYYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS
                                                                                        CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I.; Sun, J.; Butler, J.E. 33, 3565-3573, 1994.
                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                     <KAC>
                                                                                                                                                                                                                                                                      EMBL: U03779;
                                                                                                                                                                68.9%;
70.1%;
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70.1%;
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                                                                                                                                                                                                                                                                    NID:g433123;
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                                                                                                                                                               Score 868.5; DB 2
Pred. No. 5.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 868.5; DB 2
Pred. No. 5.9e-59;
2; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                              from GB/EMBL/DDBJ
                                                                                                                                                  Mismatches
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21-Feb-1997
                                                                                                                                                                                                                                                                                                                                            IgG identified PMID:7930579
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                                                                                                                                                                                                                                                                    PIDN: AAA52217.1;
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                                                                                                                                                  32;
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                                                                                                                                               Indels
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188
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            A; Reference number:
                                                                                                                                                                                                          A; Accession: A94553
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A; Molecule type: protein
A; Residues: 4-68 GBTR>
R; Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A; Title: Structure of heavy
                                                                                                                                                                  R;Birshtein, B.K.; Hussain, Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy
                                                                                                                                                                                                                                                                                                                                             Ig gamma-2 chain C region - guinea pig c;Species: Cavia porcellus (guinea pig) C;Date: 07-May-1981 #sequence_revision C;Accession: A9453; A90352; A90359; A;Trischmann, T.M.
                                                                                                                              A; Reference number: A90352; A; Accession: A90352
                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-3 <TRI>
                                                                                                                                                                                                                                                                                                    submitted to the Atlas, April 1975 A; Reference number: A94553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma 4 chain constant region - pig (fragment) C; Species: Sus scrofa domestica (domestic pig) C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 C; Accession: 147162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: immunoglobulin C F;82-151/Domain: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Five putative subclasses of swine A; Reference number: I47158; MUID:95015845; A; Accession: I47162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kacskovics, I.; Sun, J.;
J. Immunol. 153, 3565-3573,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-277 <KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSFGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQTREPQVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THTCPPCP-APELLG-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVDGTYFLYSKLAVDKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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A90359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: U03782; NID: g433129; PIDN: AAA52220.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Butler, J.E., 1994
chain from strain 13 guinea MUID:71058486; PMID:5538616
                                                                                                                                                                                                               Q.Z.; Cebra,
                                                                                                                                                    chain from strain 13 guinea MUID:71058471; PMID:5538606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 865; DB 2;
Pred. No. 8.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                            pig
pig)
                                                                                                                                                                                                                                                                                                                                                                      A90384;
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                                                                                                                                                                                                                                                                                                                                                                 07-May-1981 #text_change 16-Jul-1999
90384; A90385; A02151
                                                                                                                                                                                                                   J.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
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                  pig
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                    immunoglobulin-G(2).
                                                                                                                                                                    immunoglobulin-G(2).
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RESULT 15

147158

147158
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 14718
R;Racskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03778; NID:9433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain light guinea pigs.
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C:Superfamily: immunoglobulin cregion; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin consists immunoglobulin homology <IMIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 134-226 <TRA>
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
Biochemistry 13, tructure of the C-H3 homology region from guinea A;Title: Primary structure of the C-H3 homology region from guinea A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 69-133; 312-329 < TUR>
R; Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NWYVDGYEVHNYKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPPIEDADGSYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISKTKGAPRMPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.1%; Score 858; DB 1; 67.4%; Pred. No. 3.8e-58; tive 28; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                 cDNA sequences
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A:Gene: IgG1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
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TFFLYSKLAVDKARWDHGDKFECAVMHEALHNHYTQKSISKTQGK 328
              SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                   EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDG
                                                                             EPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO -- PENNYKTTPPVLDSVG
                                                                                                                                                                                                                      Conservative
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Search completed: July 15, 2003, 06:59:31 Job time: 14.4523 secs

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Title:
Perfect score:
Sequence:
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GCB_RAT
GC3_MOUSE
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GCA_RABIT
EPC_HUMAN
MUCH_HUMAN
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ALIGNMENTS

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"The covalent structure of a human gamma G-immunoglobulin. X.	[NE=71064027; PubMe	DISULFIDE BONDS.	Hoppe-Seyler's 2. Physiol. Chem. 364:713-747(1983).	bulin IgG1 K	"Three-dimensional structure determination of antibodies. Primary	MEDLINE=83289131; PubMed=6884994;	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.	HOPPE-SEYTER'S 2. FNYSIOI. CHEM. 33/:13/1-1004(19/0). [5]	peptides and discussion of the complete structure.";	chymotryptic peptides of the H-chain, alignment of the tryptic	"The rule of antibody structure. The primary structure of a monoclonal IdG1 immunodlobulin (myeloma protein Nie). III. The		MEDLINE=77070269; PubMed=826475;	[4]	Biochemistry 9:3171-3181(1970).	covalent structure of a human gamma G-imm	nan G.M.;	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,	MEDITUS=71064025: PubMed=5530842:	[3]	chemistry 9:3161-3170(1970).	in cyanogen bromide fragments H1-H4.";	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.T. Edolman G.M.:	; PubMed=5489771;		NUCLEIC ACIDS RES. IU:40/1-40/9(I982).	leotide sequence c	Ellison J.W., Berson B.J., Hood L.E.;	SEQUENCE FACIN N.A. MEDITNE=82274238: PubMed=6287432:	[1]	I_TaxID=9606;	Primates; Catarrhini; Hominidae;		HG1.	chain C region.	(Rel. 01,	01, Created)	GC1 HUMAN STANDARD: PRT: 330 AA.	T 1

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Biochemistry 20:2361-2370(1981).
-!- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEOUENCES HAVE THE MARKER & THE G1M (NUN-1) MARKERS.
-!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
-!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF INTSCELLANEOUS: EU ALSO DIFFERS INTSCELLANEOUS: EU ALSO DIFF
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STRAND
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Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGCl; 2.
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MEDLINE-81208100; PubMed-7236608;
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Biochemistry 9:3188~3196(1970).
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; 1FC1; 15-JUL-92.
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IGHG3.
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P01860;
SEQUENCE (DISEASE PROTEIN WIS).

MEDITINE=81021548; PubMed=6774747;

Frangione B., Rosenwasser E., Prelli F., Franklin I
"Primary structure of human gamma 3 immunoglobulin
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
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gene deletion model.";
gene deletion model.";
proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

1. SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION
NORMALLY PRESENT IN THE HINGE REGION.

1. MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS 1
1. MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 12-97 (PROTEIN WIS).

MEDLINE-77118561; PubMed-402363;

Michaelsen T.E., Frangione B., Franklin E.C.;

"Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.";

J. Biol. Chem. 252:883-889(1977).
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REVISIONS
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                                                                                                                                                         SMART; SM00410; IG_like; 1.
SMART; SM00407; IGCl; 1.
PROSITE; PS00290; IG_MHC; 1
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Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence
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MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FOR OR ANOTHER GAMMA CHAIN SUBCLASS.

MISCELLANEOUS: THE HINGE RECION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15 RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
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MISCELLANEOUS: DISEASE PROTEIN
OF THE CH1 REGION, AND PART OF
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                                                                                                                                                   SEQUENCE OF 2-326 FROM MEDLINE-82197621; PubMe
                                                                                                                                                                                             Mammalia; Eutheria;
NCBI_TaxID=9606;
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MEDLINE=83001943; PubMed=6811139; Takahashi N., Ueda S., Obata M., "Structure of human immunoglobuli

immunoglobulin

Nikaido

Т., genes:

Nakai

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(ai S., Honjo implications

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SEQUENCE OF 88-115 TISSUE=Fetal liver;

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constant region genes.";
Acad. Sci. U.S.A. 79:1984-1988(1982)

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Hofmann T., Parr D.M.;
"A note of the amino acid sequence of mmunoglobulins gamma chains.";
"munoglobulins gamma chains.";
"A note of 16:923-925(1979).
InterPro; IPR003006; 1
InterPro; IPR003597; 1
InterPro; IPR003600; 1
Pfam; PF00047; ig; 3.
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MEDLINE=69064124; PubMed=5782707;
METANGIONE B., Milstein C., Pink J.R.L.
"Structural studies of immunoglobulin
Nature 221:145-148(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Milstein C., Frangione B.; "Disulphide bridges of the heavy chain Biochem. J. 121:217-225(1971).
                                                                                                                      MIM;
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HSSP; P01857; 1FC1.
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Cell 29:671-679(1982)
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MEDLINE=72033500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of the immunoglobulins.";
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J. Biochem. 57:758-767(1979).
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                                                                                                                                            HGNC:5526;
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1 T., Parr D.M.;
ted (MAR-1980) to
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                                                                                                                                                                                                                                                                                                                                                        Bioinformatics Institute. The profit institutions as long this statement is not removed.
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PubMed=6774012;
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P01861;
21-JUL-1986
21-JUL-1986
16-OCT-2001
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MOD_RES
VARIANT
                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=83157104; PubMed=6299662;

Ellison J.W., Buxbaum J.N., Hood L.E.;

"Nucleotide sequence of a human immunoglobulin DNA 1:11-18(1981).
                                             MEDIINE-70207560; PubMed-4192699;
Pink JR.L., Buttery S.H., de Vries G.M.,
"Human immunoglobulin subclasses. Partial
constant region of a gamma 4 chain.";
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                               Biochem. J.
                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                           Homo sapiens
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IGHG4.
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SM00407; IGcl; 2.
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                               region of a gamma 4 J. 117:33-47(1970).
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C -> S (IN REF.
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REMOVED POST-TRANSI
S -> A (IN MYELOMA
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ED POST-TRANSLATIONALLY (PROBABLE)
A (IN MYELOMA PROTEINS TIL & ZIE).
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on update)
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                      MEDLINE=84030930; Pubb
Bernstein K.E., Alexar
"Nucleotide sequence of
F-I haplotype.";
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InterPro; IPR003597; Ig_cl
InterPro; IPR003600
                                                                                                                                                                                                            GC_RABIT STANDARD; PRT; 323 AA. P01870; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15 gamma chain C_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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NON_TER
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
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Pfam; PF00047; ig; 3.
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                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                   SEQUENCE FROM N.A.
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buropean Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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                                        0; PubMed=6313520;
Alexander C.B., M
uence of a rabbit
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90.5%;
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Pred. No. 3.4e
11; Mismatches
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MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.

"Sequence studies of the Fd section
immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes."; Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr.,
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127,
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SEQUENCE OF 1-128.
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          Biochemistry 10:26-31(1971).
                                              DISULFIDE BONDS.
MEDLINE-71058474;
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                                                                                             Trischmann T.M., 
"Primary structum
                                                                                                             SEQUENCE OF 227-31
MEDLINE=75036073;
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                            Oliveira B., Lamm M.E.
"Interchain disulfide
                                                                                                                                           Biochemistry 13:4796-4803(1974).
                                                                                                                                                      antibodies."
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                                                                                                                                                                                                                                              Turner K.J., Cebra J.J.;
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MEDLINE=71058486; PubMed=5538616;
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SMART; SM00407; IGc1; 2.
                                                                                                                               Brueggemann M.;
"Evolution of the rat
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157; Conserv
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                                                                                                                                                                                                                                                                                                             PS00290;
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                                                                                                                                                                                                                                                                                                                                                                                                 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT
                                                                                                                                                                                                                                                                                                                                                                                                                           ZPBPC----
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                                                                                                                                                                                                                                                                                                                                                 ISKTKGAPRMPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00290;
                                                                                                                                                                                                                  (Rel. 17, Created)
(Rel. 17, Last sequence up
(Rel. 38, Last annotation
chain C region.
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domain;
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79
105
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210
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308
36074
                                      IG_MHC;
                                                                                                                                                    PubMed=3149946;
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                                                                       Ig_MHC.
Ig_cl.
Ig_like.
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67.4%;
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                           Immunoglobulin
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Pred. No. 1.6e
28; Mismatches
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          INTERCHAIN
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                 PRT;
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                           region
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.6e-63;
                                                                                                                                                                                                                                                                 B
                                                                                                                                 heavy-chain
                                                                                                                                                                                        Muridae;
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                                                                                                                                                                                       Murinae;
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          CHAIN).
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                                                                                                                                 family."
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Gaps

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Best Local S
Matches 145
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GC3_MOUSE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    P22436;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
19 Jamma-3 Chain C region, secreted for
                                                                                                                                         HSSP;
                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions of
use by non-profit institutions its content is in
modified and this statement is not removed. Usage by and for com-
entities requires a license agreement (See http://www.isb-sib.ch/an
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     EMBO
                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                         Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
                                                                                                                                                                                                                                                                            Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constar
                                                                                                      Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                 Transmembrane;
                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                              MEDLINE=85027161; PubMed=6092053;
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                       DOMAIN
                                                     Immunoglobulin domain; Immunoglobulin C region;
                                                                                                                                                                                                                                                                     J. 3:2041-2046(1984).
                                                                                                                                                    B02156; G3MSC.
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                                                                                                                                                              J00451;
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                                                                 PS00290;
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 98
114
                                          Alternative splicing.
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Rodentia;
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Pred. No. 8.1e
84; Mismatches
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INTERCHAIN
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 HINGE.
                        CH1.
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Sciurognathi;
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on update)
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HTIW)
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thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                               constant
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.le-60;
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RESULT 9
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                         Wall R.;
                                 InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_lik
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-85027161; PubMed=6092053;

Wels J.A., Word C.J., Rimm D., Der-Balan

Tucker P.W., Blattner F.R.;

"Structural analysis of the murine IgG3 c
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 3
15-JUL-1999 (Rel. 3
Ig gamma-3 chain C
                                                                                                           EMBL; J00451; AAB59655.1;
EMBL; V01526; CAA24767.1;
PIR; A02155; G3MSM.
HSSP; P01857; 1FC1.
                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               "The
                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 328-398 FROM MEDLINE=84041483; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P03987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GC3M_MOUSE
                                                                                                                                                                                                                                                                     Nucleic Acids Res. 11:6775-6785(1983).
                        PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1986 (Rel.
              Immunoglobulin
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                                                          ; IPR003006; Ig_MHC.
; IPR003597; Ig_c1.
; IPR003600; Ig_like.
00047; ig; 3.
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329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                    Clayton
Alternative splicing
              domain;
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19, Last
38, Last
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36228 MW;
                                                                                                                                                                                                                                                                                             the mouse immunoglobulin in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region,
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64.7%;
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              Immunoglobulin C
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            region;
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            Glycoprotein;
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murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).

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GC1_MOUSE
ID GC1_W PO186
AC P0186
DT 21-JU
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(1)
SEQUENCE FROM N.A.
MEDLINE=80045036; PubMe
"Tanio T., Obata M., Yau
"Tanio T., Obata M., Yau
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21-JUL-1986 (Rel. 0)
30-MAY-2000 (Rel. 39
Ig gamma-1 chain C
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                SEQUENCE (MYELOMA MEDLINE=78242288; Adetugbo K.;
                                                                                                                                                                                                            *Immunoglobulin gamma cloned in a bacterial Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                 SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC MEDLINE=80202559; PubMed=6769752; Obata M., Yamawaki-Kataoka Y., Takahashi N., Katao
                                                                                                                                                                                                                                                                                                                                                              gamma
Cell 1
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                                                                                                                                                                                                                                                                                                                                                                                                            Honjo T., Obata M.,
Takahashi N., Mano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                          "Sequence analysis heavy chain.";
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of immunoglobulin subclasses.
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HINGE.
CH2.
CH3.
POTENTIAL.
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E -> G (IN REF. 2).
E -> G (IN REF. 2).
F -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
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cDNA encoding
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Pred. No. 8.9e-59;
5; Mismatches 41
                                                                                                                                                                                                                                   chain gene:
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EMBL; V00793; CAA24175.1;
EMBL; V00793; CAA24175.1;
EMBL; V00795; CAA24175.1;
EMBL; V00795; CAA24176.1;
PIR; A02159; GIMS.
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InterPro; IPR003006; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003597; Ig.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 2
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Svasti T
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GlycoSuiteDB; P01868;
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Immunoglobulin dom
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                                                                             PRDCG----CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQ
        PPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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QPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK
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58.4%;
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Pred. No. 6.7e-58;
7; Mismatches 41
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INTERCHAIN
INTERCHAIN
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N -> D (IN REF. 3).
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CH3.
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AC P01869
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DE 19 gam
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GC1_RAT

P20759;

01-FEB-1991 (Rel. 17, Created)

01-FEB-1991 (Rel. 17, Last sequence up

15-JUL-1999 (Rel. 38, Last annotation

Ig gamma-1 chain C region.
                         GCIM_MOUSE STANDARD; PR P01869; P01869; P1-1986 (Rel. 01, Created) 01-AUG-1991 (Rel. 19, Last seque 30-MAY-2000 (Rel. 39, Last annot 19 gamma-1 chain C region, membr
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                              SEQUENCE
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                 Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
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Gene 74:473-482(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                     TPPTMDTDGSYFLYSKLNVKKEKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK 326
                                                                                                                                                          PS00290;
                                                                                                                                  TPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                HFSWFVDDVEVHTAQTRPPEEQFNSTFRSVSELPILHQDWLNGRTFRCKVTSAAFPSPIE
                                                                                                                                                                                                          KFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIE
                                                                                                                                                                                                                                                    PKSCDKTHTCPPCPAPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
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IPR003597;
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113 219
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35946 MW;
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                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             domain;
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    Last sequence up
    Last annotation

Rodentia;
         Chordata;
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58.5%;
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                            membrane-bound
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; 013BAB45EF49B9DA CRC64;
                                                                                                                                                                                                                                                                                  Score 784.5;
Pred. No. 1.
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HINGE.
CH2.
CH3.
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Sciurognathi;
Sciurognathi;
         Craniata;
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ion update)
                                            update)
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1.7e-57;
                                   update)
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thi; Muridae; Murinae; Rat
         Vertebrata;
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 Muridae;
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         Euteleostomi;
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Murinae;
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Honjo T., Obata M., Yam
Takahashi N., Mano Y.;
"Cloning and complete n
gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                             MGD; MGI:96446; Igh-4.
InterPro; IPR003006; Ig
InterPro; IPR003597; Ig
InterPro; IPR003597; Ig
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGC1; 2
PROSITE; PS00290; IG_MH
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-i- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA

SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED

GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE

BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED

IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-44 FROM N.A. MEDLINE=82222190; PubMed=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rogers J., Choi E., So
Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved transmembrane
domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=82197626; PubMed=6804950;
Tyler B.M., Cowman A.F., Gerondakis
"mRNA for surface immunoglobulin gan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=80045036; PubMed=115593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
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Cell 26:19-27(1981).
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                                                                                                                                                                    mmunoglobulin
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B02159; GIMSM.
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splicing; Transmembrane
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             (GLCNAC
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28-residue
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HTIW)
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RESULT 13
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                                                                                                                                                           InterPro: IPR003597; Ig_c1.
InterPro: IPR003600; Ig_like.
Pfam; PF00047; ig; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                  NON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=88166903; PubMed=3127222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Métazoa; Chórdata;
Mammalia; Eutheria; Rodentia;
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15-JUL-1999 (Rel.
Ig gamma-2C chain
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                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence of a rat immunoglobulin gamma 2c heavy region cDNA: extensive homology to mouse gamma 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brueggemann M., Delmastro-Galfre P.,
                                                                                                                                               [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation een the Swiss Institute. There are no restrictions on its European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 18:317-319(1988).
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135; Conser
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                                                                                                                                                                                                                                                                                                                                       equires a license agreement (See http://www.email to license@isb-sib.ch).
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                                                                                                                                               domain;
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58.2%;
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annotation update)
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Pred. No. 2.26
7; Mismatches
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CYTOPLASMIC (POTENTIAL).
, 4CC88343B7A1CE27 CRC64;
    INTERCHAIN INTERCHAIN
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Sciurognathi; Muridae
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mma 2c heavy chain constant
ouse gamma 3.";
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    HTIW)
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                                                                                                                                                                                                                          family.";
   DISULFIDE BONDS.
MEDLINE=73056887; PubMed=4565406;
de Preval C., Fougereau M.;
"Determination of the primary str
                                                                                                                                                                                                                                                                                                                                                 "The complete nucleotide sequence and evolution of heavy chain genes sequence mediated domain transfer
                                                                             Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. If for the evolution of immunoglobulin structure and function. J. Biochem. 43:423-435(1974).
                                                                                                                                                                           MYELOMA PROTEIN MOPC 173
                                                                                                                                                                                                           Proc.
                                                                                                                                                                                                                                     MEDLINE-81223894; PubMed-6787604;
Ollo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma suggests that exons can be exchanged between genes in a
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-81198976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated
Balb/C gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=81076554; PubMed=6777755;
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Yamawaki-Kataoka Y., Miyata T., F
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STRAIN=C57BL/6;
STRAIN=C57BL/6;
MEDLINE=82037861; PubMed=6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B.
"Multiple differences between the nucleic acid
"Multiple differences between the mouse.";
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 gamma-2A chain C region, B allele.
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InterPro; IPR003600; Ig_like.
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SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send, an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain Fc regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78.4031-4035(1981).
-i- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J00479; -; NOT_ANNOTATED_CDS. PIR; A02153; G2MSAB.
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                          SVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                         CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
SDGSYFMYSKLRVQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLGK
                                                                                                               RGPVRAPQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLD
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60.1%;
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Pred. No. 1.
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1 EPKSCDKTHTCPPCP
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1: sp_archea:*
2: sp_bacteria
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                                   O8tc77 homo sapien
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Q8tc63 homo sapien
Q95m34 equus cabal
Q8tr3v9 mus musculu
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Q90530	Q99LA6	Q8VCV5	Q99M22	Q8WY24	Q9NPP6	Q9BRV0	Q96DK0	Q91XE1	Q91WP5	Q96KX8	Q96K68	Q9UP60	Q8VCX4	Q91WR1	Q8VEA0	Q91x92	Q91WT1	Q91WT3	Q9DCD9	Q99KA4	Q91Z07	Q90544	Q96AA6	Q96GA6	Q8WUK1	Q96EY0	Q8WUX4	Q8VCX7
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ALIGNMENTS

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181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232	121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180 	61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120 	1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKF 60 	Query Match 97.2%; Score 1225; DB 4; Length 471; Best Local Similarity 97.0%; Pred. No. 4.8e-108; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	OBTC77 PRELIMINARY; PRT; 471 AA. QSTC77; QSTC	+

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420

PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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PROSITE: PS00022; EGF_1; UNKNOWN_1.
PROSITE: PS01186; EGF_2; UNKNOWN_1.
PROSITE: PS01187; EGF_CA; UNKNOWN_1.
PROSITE: PS0011; GLU_CARBOXYLATION; UNKNOWN_1.
PROSITE: PS00290; IG_MHC; UNKNOWN_1.
PROSITE: PS00290; IG_MHC; UNKNOWN_1.
PROSITE: PS00240; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE: PS00135; TRYPSIN_EGR; UNKNOWN_1.
PROSITE: PS00135; TRYPSIN_EGR; UNKNOWN_1.
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InterPro; IPR001254; S
InterPro; IPR000294; V
Pfam; PF00008.
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Ol-MAR-2002 (TrEMBLrel. 20, La
Factor VII active site mutant
Homo sapiens (Human'
               Q8TC63;
Q8TC63;
01-JUN-2002
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InterPro; IPR000561; EGF-1ike.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001306; Ig_MHC.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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n; PF00594; 91a; 1.
n; PF00047; ig; 2.
n; PF00089; trypsin; 1.
RT; SM00181; EGF; 2.
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Pred. No. 8.2e
3; Mismatches
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Q95M34;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
                                      Pfam; PF0
PROSITE;
NON_TER
SEQUENCE
                                                                                    "Organization of the equine immunoglobulin genes. III. Alignment of c-mu, c-gamma, c-c Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-98383416; PubMed-9717671;
MEDLINE-98383416; Sheoran A.,
                                                                                                                                                                                                                  Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                          Wagner B., Overesch G.,
Leibold W., Radbruch A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, La 01-JUN-2002 (TrEMBLrel. 21, La Hypothetical 52.0 kDa protein.
                                                                                                                                                                         Submitted
                                                                                                                                                                                  Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2002) to the EMBL; BC025985; AAH25985.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      Immunogobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                    432
 al Similarity
157; Conser
                                                                   Pro; IPR003006; PF00047; ig; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
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                                                                                                                                                                                                                                                                                                                                                                             LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                      LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
                                                                                                                                                                        (DEC-2000)
                                                                                                                                                                                                                                                                    1 (TrEMBLrel. 19, 0
1 (TrEMBLrel. 19, 1
2 (TrEMBLrel. 21, 1
1 gamma 1 heavy
                                       337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 protein 473 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
                                       AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
         69.6%;
                                       37438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51986 MW;
                                                                          Ig_MHC
                                                                                                                                                                         6
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90.5%;
                                                                                                                                                                        the EMBL/GenBank/DDBJ

    Last sequence update)
    Last annotation update)

                                       MW,
                                                       UNKNOWN_2.
 36;
                                                                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                                      chain
                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1097; DB 4;
Pred. No. 7.1e-96;
                    Score 877.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                    PRT;
                                      A60BF2B01DEFD1F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E29920B09BA369F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
 Mismatches
                                                                                                                                                                                                                                                                    sequence update)
annotation update)
constant region
          No.
                                                                                                                                    Holmes
                                                                                                       c-epsilon
 es 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
                    DΒ
                                                                                                       heavy chain constant region epsilon and c-alpha genes.";
                                                                                                                                   M., Richards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                   6;
                                                                                                                                                                        databases
                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                  Length
 Indels
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                                                                                                                                                                                                                                                                                                                                                                    473
                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                    337;
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2;
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databases

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RESULT
Q99LC4
ID Q99LC4
AC Q9
AC Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
DT 01
DT 02
AC Q9

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QA
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Best Local
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                                                                                                                                                                                                  Q99LC4;
Q99LC4;
01-JUN-2001
01-JUN-2001
01-JUN-2002
Similar to R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBR3V9:
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2002) to the EMBL; BC024405; AAH24405.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8R3V9
                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YMDGVEVRTATTRFKEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTKGRSQEPQVYVLAPHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSWFVDDVEVHTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein.
                                                                                                                                                                                                            RIKEN
                                                                                                                                                                                                     (TTEMBLrel. 17, Created)
(TTEMBLrel. 17, Last sequence up
(TTEMBLrel. 21, Last annotation
RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQ
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59.2%;
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 798.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534793F155D05457 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑA
                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11;
                                                                              Muridae;
                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Murinae; Mus
                                                                          Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
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Q9R1A4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
                                                                                                                                                                                              SEQUENCE FROM N.A.

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S
Fall Stophitted (MAX-1999) to the EMBL/GenBank/DDBJ date
EMBL; AF152372; AAD40243.1; -.

EMBL; AF152372; AAD4024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003600; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 4.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_MHC; UNKNOWN_1.
SEQUENCE 463 AA; 51007 MW; EAA674C
      PROSITE;
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Gammal heavy chain of Mab7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2001)
EMBL; BC003435; AAH0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg
                                                                                                                                    Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9R1A4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9R1A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:96446; Igh-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01842; 7FAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEK 119
                                                                                                         PS00290;
437
437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001) to the AAH03435.1;
                                                                                                      IG_MHC;
          48142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.1%;
                                                                                                         UNKNOWN_1
          MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 795.5;
Pred. No. 3.1e
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAA674C6BBC30783 CRC64;
          5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K.M., Misra S.;
white pine blister rust monoclonal
chains) and construction of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1e-67;
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on update)
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463 232

410

350

databases

Euteleostomi; ; Murinae; Mus

DB 11; 41;

Indels Length

9,

Gaps

59

290

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                                                                                                                                                                                            RA Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Datawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Sakai K., Okido T., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Asasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashtzaki Y..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
          SMART; SM00409;
SMART; SM00407;
SMART; SM00406;
SMART; SM00410;
                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK007918; BABE2349.1; -.
HSSP; P01842; 7FAB.
MGD; MGI:96443; Igh-1.
                                                                                InterPro;
                                                                                                                  InterPro;
                                                                                                                                                                                        Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21085660;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9D8L4
                                                                                            InterPro;
                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9D8L4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [6H-1 OR 1810060009RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                          PF00047; ig; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
                                                     918;

942; 7FAB.

96443; Igh-1.

0; IPR003599; Ig.

1PR003597; Ig.c1.

1PR003600; Ig.like.

193006; Ig.MHC.

1940:
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                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.8%; illarity 58.4%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
          IG; 2.
IGc1; 3.
IGv; 1.
IG_like;
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11217851;
IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 791.5; DB 1
Pred. No. 6.9e-67;
7; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 437;
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; Murinae; Mus.
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                                                                                                                                                                                                                         K. -F.,
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                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                       Pfam;
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Query Match
Best Local S
Matches 141
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SMART;
SMART;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00290; SEQUENCE 468 AA.
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Pfam; PF00047; ig; 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     Local Local 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00409;
SM00407;
SM00406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treu (FEB-2001) to the EMBL/GenBank/DDBJ databases BC003878; AAH03878.1; -.
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138; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
YEMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
                                  FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                  RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS
                                                                                                                                REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS
                                                                                                                                                                                                          CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQP
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IPR003600;
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19; 19; 3.
19; 16; 2.
20; 16cl; 3.
406; IGV; 1.
0410; IG_like; 1.
0410; IG_MHC; UNKNOWN_1.
050290; IG_MHC; UNKNOWN_1.
0502900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 AA;
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Rodentia;
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Ig_like.
Ig_MHC.
Ig_v.
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Pred. No. 6.1e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9DED57A514475FBB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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        468
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RESULT 10
099L25

ID Q99L2
AC Q99L2
AC Q99L2
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT SIMI
OC EUKA
OC MAMM
OC MA
RESULT
1091205
AC 05
AC 
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Qd
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Best Local
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IG; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_MIC; UNKNO
PROSITE; PS00290; IG_MIC; UNKNO
SEQUENCE 473 AA; 52449 MW;
                                                                                                                                                                                                                                                                                                                O91Z05; PRELIMINARY;
O91Z05;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TREMBLrel. 2
AU044919.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_VHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003596 Pfam; PF00047; 1g;
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Submitted (FEB-2001)
   Strausberg R.;
Submitted (JUL-2001) to the
EMBL; BC010327; AAH10327.1;
MGD; MGI:2144967; AU044919.
                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC003888; AAI
HSSP; P01842; 7FAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPPCKCPAPNLLGCPSVEIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPKGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.3%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the
                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                 19,
19,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNKNOWN_1.
MW; BE9889B7986DA155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 772; DB
Pred. No. 5.5e
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                  Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473
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thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
5.5e-65;
                                                                                                                                                                                                                                                      Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                         Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                         Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                         Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369
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Q9BSZ1
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RESULT
Q8R3H6
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                                                     δÃ
RESULT 13
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Best Local S
Matches 140
                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                            Q8R3H6;
Q1-JUN-2002 (TrEMBLrel. 21, Last
Q1-JUN-2002 (TrEMBLrel. 21, Last
Q1-JUN-2002 (TrEMBLrel. 21, Last
Hypothetical 51.7 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 3.

PROSITE; PS00190; CYTOCHROM
PROSITE; PS00290; IG_MHC; U
Hypothetical protein.
SEQUENCE 473 AA; 51946 M
                                                                                                                                                                                                                                                                          Submitted (MAR-2002) to the EMBL; BC025447; AAH25447.1; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8R3H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000345; CytC_heme_bind
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                               Strausberg
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415
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                                   416
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                                                                                                                                                                                                                       140;
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                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                                                         DPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDL
                                                                                                                                      EDPEVKENWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKAL
                                                                                                                                                                                   EPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDPEVKENWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKAL
                                                                             EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE
                               ENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                NNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                         EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE
                                                                                                                                                                                                                                                                  al protein.
474 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOCHROME_C; UNKNOWN_1.
IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                           Chordata; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51946 MW;
                                                                                                                                                                                                                                                                   51748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.7%;
                                                                                                                                                                                                                                59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 752.5; DB 1
Pred. No. 3.9e-63;
                                                                                                                                                                                                                     Pred. No. 3.906; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF625F008932AF12
                                                                                                                                                                                                                                                                  8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        474
                                                                                                                                                                                                                                   3.9e-63;
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                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                     56;
                                                                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473
                                   474
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Q9BSZ1

PRELIMINARY;

PRT;

375

B

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RESULT 14
Q9BQB
ID Q9BQB
ID Q9BQB
AC Q9BQB
DT 01-JU
DT 01-DE
DE Unkno
OS HOMO
OC EUKAR
OC MAINWAA
OC NCBI_
RN [1]
RP SEQUE
RC TISSU
RA STRAU
RL SUBMI
RL SUBMI
RL SUBMI
RA STRAU
RL SUBMI
RA STRAU
RA STR
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003600; I
InterPro; IPR003006; I
Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1;
                       Submitted (JAN-2001) to the EMBL; BC006180; AAH06180.1; EMBL; BC001872; AAH01872.1; H$SP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat update)
Unknown (protein for MGC:1905) (protein for MGC:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9BSZ1;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence up
O1-DEC-2001 (TrEMBLrel. 19, Last annotation
Hypothetical 41.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BQB8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein SEQUENCE 375 AA; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00407; IGC1; 3.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2001)
EMBL; BC004476; AAHO
HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                              Strausberg R.;
                                                                                                                                      TISSUE-LYMPH
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                             Strausberg
                                                                                                                                                                                                                                                  TISSUE=MUSCLE;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            о во в
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
    [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SVGSFFLYSKLTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK-VQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVS
                                                                                                                                                                                                       (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH04476.1;
                                                                                                                                                                                                                                                                                                                                             Primates;
                                                                                                                                                                                                                                                                                                                                                              Chordata;
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33.6%;
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                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                       EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 347;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                         Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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9.8e-25;
nes 86;
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SMART; SM00407; ĪGc1; 4.
SMART; SM00406; ĪGv; 1.
SMART; SM00410; ĪG_like; 1.
PROSITE; PS00290; ĪG_MHC; U
SEQUENCE 597 AA; 65300 M
                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 597 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR003006; Ig_MHC.
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Mammalia; Eutheria;
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InterPro; IPR003006;
InterPro; IPR003596;
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PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=B-CELL;
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les 72; Conserv
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72; Conserv
NLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVS
                                                                                  VELEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNST
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                                        T-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SVGSFFLYSKLTVD
                                                                                                                                                                        VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNAT
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(TremBLrel 19, Last seq
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                                                                                                                                                                                                                                                             Conservative
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Pred. No. 1.8e
48; Mismatches
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Pred. No. 1.8e-24;
8; Mismatches 86
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86;
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Match
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Gapop 10.0 , Gapext 0.5
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      A_Geneseq_101002:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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  AAW26232
AAB28690
AAY28697
AAB80897
AAB15347
AAB15347
AAB19463
ABB09463
AAB24154
AAB47590
AAR91806
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Compugen Ltd.
Human IgG1 hinge/F
Human IgGgammal hi
Human partial IgG1
Human igggammal hi
Human immunoglobul
Human immunoglobul
Human immunoglobul
Protein from pCd51
Fusion protein of
Human immunoglobul
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	97.2																																	
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20	23	22	19	14	23	21																	19	19	19	10	10	14	21	23	23	23	23	22
AAY30201	810	AAE12715	AAW49816	AAR43339	AAM49203	AAB28694	AAY31669	AAW05829	AAY24153	AAW10550	AAB28692	AAW10552	AAR26530		AAW14765	AAW14764	AAB28693	AAU97108	AAY15123	AAW18575	AAW18574	ABB07681	AAW49073	AAW83962	9	355	191	4368	AAY91106	85	ω	9	ABB81641	AAB04071
Heavy chain sequen	B7-related protein	Human recombinant	Amino acid sequenc	Completely humanis	Ħ	1 (99-	10	sed 1D10	ne LOX-1	pep	Fc-huAGP-1 (95-281	acid	o	Fc-muAGP-1 (120-29	Human soluble kit	Human soluble kit	GP-1	Mouse MK61-human I	~	Aggrecanase artifi	tif			=	c pepti	hun	nce of the	kappa	Human TR-Fc-delta-		Human immunoglobul	death doma	IgG gamma	Zcytor 10::IqG qam

ALIGNMENTS

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WPI; 1997-402624/37. N-PSDB; AAT80158. Recombinant protein expression system for fusion protein production - useful for high quantity production of authentic recombinant proteins	31-JAN-1996; 96US-0595043. (TECH-) TECHNOLOGENE INC. Sgarlato GD;	W09728272-A1. 07-AUG-1997. 31-JAN-1997; 97WO-US01470.	Human IgG1 hinge/Fc region. Fusion protein; hydrophilic spacer; recombinant; expression system; carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc. Homo sapiens.	RESULT 1 AAW26232 ID AAW26232 standard; Protein; 232 AA. XX AC AAW26232; XX T 16-MAR-1998 (first entry)

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RESULT 2
AAB28690
ID AAB28690
ID AAB28690
AC AAB2
AC AAB2
AC AAB2
AC AAB2
AC Huma
XX Huma
KW Huma
KW Antii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-terminus, of a first domain comprising a protein of interest, a second domain comprising a hydrophilic spacer and an affinity domain, each domain comprising amino acid residues. The present sequence represents the hinge-Fc region of human IgG1, used in example 3 of the present invention. The recombinant vector is used for the production of authentic recombinant proteins of interest. The method of the invention is useful for the expression of fusion proteins capable of isolation by affinity chromatography in pro- or eukaryotic cells. This method allows for the efficient cleavage and generation of authentic proteins of interest that do not contain extraneous (i.e. non-naturally occurring)
WPI; 2000-665240/64
                                                              Hsu H,
                                                                                                                                                                                   16-APR-1999;
                                                                                                                                                                                                                                            24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arteriosclerosis; IgGgammal.
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                                                                                                                                                                                                                                                                                                       26-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB28690 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                        Meng S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                            2000WO-US08004
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                                                                                                                       INC
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97.08;
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Pred. No. 2.1e-90;
3; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein proliferative d disorders -
                                                                                                                                                                                                                                                                                                                                                          include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AQP-1 containing fusion proteins have increased biological activity composite to the AQP-1 containing fusion proteins have increased
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence was used in the production of AGP-1 fusion proteins. AGP-1 is a type II transmembrane protein. The fusion proteins comprise an Fc immunoglobulin region fused to the N-terminal portion of the AGP-1 protein. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders
                                                                                                                                                                                                                                                                                                                                  prior art
                                                                                                                                                                                                                                                                                                                                                 may also be treated.
biological activity
                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                        Local
121
                                                                           121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                       61
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                                                                                                                                                    61
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225; Conser
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                                                                                                                                                                           EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
                                                                                                                   Fig
                                                           ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                  therapies
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of AGP-1 protein disorders, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93pp;
                                                                                                                                                                                                                                                                                                                                               compared
                                                                                                                                                                                                                                                       97.2%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                         Score 1225; DB 21
Pred. No. 2.1e-90;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                              to the soluble AGP-1 proteins used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and an Fc region, used to treat disorders, and virally-induced
                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                          Indels
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AAY72915
13-JUN-2001
                                                                                                                                             AAY72915 standard; Protein;
                                                                                                          partial IgG1 protein comprising hinge,
                                                                                     fusion protein; osteoprotegerin;
y; bone loss; osteoporosis; Paget
alcaemia; osteopenia; osteonecros;
                                                                                                                      (first entry)
                                                                                                                                             232
                                                                                                 OPG;
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Dunstan

CR,

Wooden

Mann

MB

(AMGE-) AMGEN INC

WO200118203-A1

Homo sapiens

18-AUG-2000; 15-MAR-2001

2000WO-US22797

osteolytic metastasis; prosthetic loosening;

rosis; Paget's disease; osteomyeliti osteonecrosis; rheumatoid arthritis

FC CH2 and

protein;

osteopathic;

CH3 regions.

periodontal.

therapy; bone lo hypercalcaemia;

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Matches 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone loss, osteolytic metastasis and/or prosthetic loosening. The present sequence is partial human immunoglobulin G (Ig G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis -
                                                                                                                                                                                                                                                                                                                                                                                                  lytic bone disease; multiple myeloma; immunoglobulin; osteosclerotic bone metastasis; OPG; osteoprotegrin; osteoclast formation inhibition; bone resorption inhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB80897 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein comprising
                                                                                                                    03-SEP-1999;
                                                                                                                                                                       18-AUG-2000; 2000WO-US22806
                                                                                                                                                                                                                                                                                         WO200117543-A2
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human IgGgammal hinge, CH2 and CH3 regions
                                                           (AMGE-) AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IgGgamma1; anticancer; Antimetastatic; Osteogenic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                              INC.
                                                                                                                    99US-0389545
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97.08;
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Pred. No. 2.1e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                           inhibition
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1;
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polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preventing or treating lytic bone diseases, with cancer or metastasis, by administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-265936/27.
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                                                                                                                                                       21-APR-2000; 2000US-0559001
                                                                                                                                                                                                                                                            01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE15347 standard; Protein; 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion proteins can exhibit increased circulating half-lives and
                                                                                                                                                                                                         19-APR-2001;
                                                                                                    (AMGE-) AMGEN INC
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                                                     JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                              myelosuppressive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     times, thereby providing a more sustained activity.
                                                       Elliott SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 AA;
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97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Epo; haematocrit; anaemia; kidney function; IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IgG) gamma 1 constant heavy chain hinge region
                                                       Browne
                                                                                                                                                                                                                                                                                                                                                                                                              therapy; anti-viral drug;
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Pred. No.
                                                       JK,
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No. 2.1e-90;
                                                       Sitney
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Matches
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           04-JUL-2001; 2001WO-JP05788
                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                   01-JUL-2002
                                                                                                                                       Misc-difference
                                                                                                                                                                                Homo
                                                                                                                                                                                                           Protein A;
                                                                                                                                                                                                                                                                                                                          ABB09463 standard; Protein;
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                                                                   WO200204602-A1
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169
                                                                                                                                      Location/Qualifiers 168
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97.0%;
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                                                                                                                       "encoded by GAC"
                                                                                            "encoded by ACC
                                                                                                                                                                                                           IgG; antibody; human
                                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                                       acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      score 1225; DB 23;
Pred. No. 2.1e-90;
3; Mismatches 4;
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Best Local
                                                                       neuroprotective; antirheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia qr multiple sclerosis; insulin dependent diabetes mellitus; asthma: rheumatoid arthritis; bronchitis; emphysema: renal disease; lymp glomerulonephritis; vasculitis; chronic lymphoid leukaemia; neph glomerulonephritis; renal nephasm; multiple myeloma; amyloidosis; hyperonephritis; renal nephasm; multiple myeloma; amyloidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a transformant yeast that can present protein A or its fragment on its cell surface. The yeast can be used for detecting or isolating the Fc part of immunoglobulin (1g)G. The yeast is useful for a stable supply of highly active catalytic antibody e.g. by screening novel functional molecules and in isolating Fc-carrying secretory proteins. The yeast of the invention is capable of adhering specifically to a combinatorial antibody library with an Fc-carrying antibody component. The current sequence represents the human IgG Fc fragment
                                              graft-versus
                                                                                                                                                                                                                                           Human immunoglobulin gammal constant region protein SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A or
                                                                                                                                                                                                                                                                                                              ABB81490
                                                                                                                                                                                                                                                                                                                                             ABB81490 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transformant yeast for stable supply of highly active catalytic antibody, comprises the capability of expressing and presenting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanaka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-2000; 2000JP-0206689.
                                                                                                                                                                                           Lmmunosuppressive; dermatological; antiinflammatory; antidiabetic;
                                                          ight chain neuropathy; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-148174/19
                                                                                                                                                                                                                                                                                                                                                                                                                             182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                              Ztnfr12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKYSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                           PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment, particularly with the ZZ domain, on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ueda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                              host disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                             tumour necrosis factor receptor; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25pp; Japanese
                                                                                                                                                                                                                                                                                                                                             Protein;
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97.0%;
                                            graft rejection; Crohn's
                                                                                                                                                                                                                                                                                                                                             251
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Pred. No. 2.
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                                                           large vessel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23;
?.1e-90;
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                                              disease
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on the cell
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                                                                                                           lymphoma;
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                                                                                                                                            gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t protein A
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                                                                                                                                                                                                                                                                                                                                               designated Zinfilz (1). (I) has cytostatic, immunosuppressive, contributions and incorpretentic, antiarthritic, antiasthmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (I) can be used for cativities, and can be used in gene therapy. (I) can be used for cinhibiting, in a mammal, the activity of a ligand that binds Ztnfrll (e.g. ZTNF4), for treating disorders and diseases associated with B cymphocytes, activated B lymphocytes or resting B lymphocytes, and for cinhibiting the proliferation of tumour cells. (I) is useful for treating gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, correnal disease such as glomerulonephritis, vasculitis, chronic lymphoid correnal disease such as glomerulonephritis, vasculitis, chronic lymphoid correnal disease, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel disease, graft-versus host conduction and cytokine production, and for modulating the immune system, for regulating B cell responses and communication. Human Zinfrlz is located to chromosome 22q13.2. The communication. Human Zinfrlz is located to chromosome 22q13.2. The communication is used in an example from the present invention.
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                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                           Matches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-2000;
20-DEC-2000;
28-JUN-2001;
29-AUG-2001;
                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-508212/54.
)B; ABN89435.
                                                            140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated human tumor necrosis factor receptor polypeptide, termed 12, useful for treating autoimmune disorders, emphysema, end renal failure or renal disease and lymphoma -
200
                         181
                                                                                          121
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                                                                                                                          80
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                                                                                                                                                                                         20
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                                                                                                                                           NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                          EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
           PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                           ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                          NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                            ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                           251
                                                                                                                                                                                                                                                         Conservative
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2000US-257131P.
2001US-301715P.
2001US-315565P.
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                                                                                                                                                                                                                                                                     97.2%;
97.0%;
                                                                                                                                                                                                                                                           ω,.
                                                                                                                                                                                                                                                    Score 1225; DB 23;
Pred. No. 2.3e-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a human tumour necrosis factor
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor
                                                                                                                                                                                                                                                       Gaps
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Matches
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Best Local
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19-DEC-1997;
09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a fusion peptide which consists of the extracellular domain of a mammalian oxidized LDL (low density lipoprotein) receptor, fused to a partial heavy chain of a mammalian immunoglobulin containing all or part of the constant region. Oxidize LDL is a denatured form of LDL occurring in patients having arteriosclerosis or hyperlipidaemia, and the fusion peptide can be used for the assay of oxidized LDL in biological samples from such patients, for the diagnosis of the disorders. It can also be used therapeutically for the prevention and treatment of arteriosclerosis hyperlipidaemia. The present sequence represents the protein from the vector DNA of pCd51neg1 comprising human IgG1 Fc region genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 92-96; 105pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion peptide for assay of oxidized LDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kakutani M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9932520-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      density lipoprotein; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-418906/35.
DB; AAX88533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      denatured; oxidised; arteriosclerosis; hyperlipidaemia;
density lipoprotein; receptor; detection; immunoglobulin
                                                                                                                                            121
                                               181
                                                                                                                                                                                               88
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                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                      ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                      NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                   EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                         PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                               NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                               ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pCd51neg1 comprising human IgG1 Fc
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97JP-0364981.
98JP-0349648.
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                                                                                                                                                                                                                                                                                                                                                                                                                97.28;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 1225; DB 20;
Pred. No. 2.4e-90;
3; Mismatches 4;
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Best Local Sim
Matches 225;
                                                                                                                                                                                                                                                                                                            This sequence represents a fusion protein which comprises the mouse heat shock antigen (HSA) fused to human IgG1 Fc. This protein may be used in the method of the invention for inhibiting destruction of tissue initiated by autoreactive T cells (aTC). The method is especially used to treat subjects suspected of having autoimmune diseases, particularly multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, psoriasis, diabetes and allergy, also transplant rejection. Transgenic mice that express human CD24 on their T cells are useful as models for testing drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting tissue destruction by autoreactive T cells, useful treating autoimmune diseases, by administering a heat-shock antigen/CD24 polypeptide or its antibody
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; psoriasis; diabetes; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SIHO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transplant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion
  10
                                                             181
                                                                                     176
                                                                                                          121
                                                                                                                                   116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-611581/70.
DB; AAH43523, AAH43524.
                                     236
                                                                                                                                                          61
                                                                                                                                                                                 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein of HSA:human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heat shock antigen;
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                     against autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OIHO AIND
                                   ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                  NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                             NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                               EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF. 115
                                                                                                                                                                                             EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                  ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                               287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 10; 34pp; English.
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US40390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ď,
                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                         97.2%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSA; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IgG1
                                                                                                                                                                                                                                          Score 1225; DB 22
Pred. No. 2.8e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal transducer;
                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aTC;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                     287;
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                                    287
                                                          232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tor
                                                                                                                                                                                                                                                                                                                                                                                                              mouse
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RESULT 11
AAB04071
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                                                                                                                                                                                   QΥ
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                                                                                                                                                                                                                              Qγ
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                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                Matches
 2cytor 10::IgG
                                                                                                                                                                                                                                                                                                                                                           The gene coding for human alkaline phosphatase is fused downstream of a gene coding for either the variable and CHI regions of an antibody heavy chain or an antibody light chain. Coexpression of the H- and L-chain sequences, one of which is fused to the AP gene, results in production of AP-labelled antibodies suitable for use in immunoassays. The present sequence is from a human IgG heavy chain constant region.
                      11-APR-2001
                                                                AAB04071
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 13-15; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant alkaline phosphatase (AP)-antibody fusion protein comprises AP fused downstream of antibody heavy or light chain, useful as immunoassay reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR91806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR91806 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TOYJ ) TOSOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP08070875-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunoglobulin gamma heavy chain constant region sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1996-203155/21.
DB; AAT27385.
                                                                                                                                           181
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                                                                                                                                                                218
                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                              225;
                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                         Similarity
                                                                standard;
                                                                                                                                 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                    NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                   ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                         ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                          NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                     PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hinge;
                                                                                                                                                                                                                                                                                                                                         329
                                                                                                                                                                                                                                                                                               Conservative
                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORP
gamma
                                                                                                                                                                                                                                                                                                                                         ΑĀ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0211035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         case; label; antibody;
fusion protein; chime;
                                                               Protein;
                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                        97.2%;
97.0%;
 fusion
peptide.
                                                                330
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                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                             Score 1225; DB 17
Pred. No. 3.2e-90;
3; Mismatches 4
                                                                A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ibody; IgG;
chimera; in
                                                                                                                                                                                                                                                                                                                  DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ımmunoassay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H-chain;
                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-region;
                                                                                                                                                                                                                                                                                                                   329;
                                                                                                                                                                                                                                                                                              0;
                                                                                                                      329
                                                                                                                                         232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH1;
                                                                                                                                                                                                                                                                                              Gaps
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Qγ
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                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                         receptor. Those cells can then be used to detect the presence of a commodulator of zcytor10 protein by culturing the cells in the presence of a test ligand and comparing levels of activity of mouse zcytor10 cc in the presence and absence of the test sample. Similarly, detection of zcytor10 receptor ligand within a test sample can be achieved. The method comprising contacting a test sample containing an amino cc acid sequence from Cysls or Gly25 to pro230 of the zcytor 10 cc cytokine receptor and detecting the binding of the polypeptide to a cligand in the sample. Specified peptide fragments of the zcytor 10 cc ytokine receptor and the methods described are used to identify cligands that stimulate the proliferation and/or development of the acytokine receptor and the methods described are used to identify cc haematopoietic, lymphoid and myeloid cells. Peptide fragments of the cytokine receptor are useful for treating lymphoid, immune, cc inflammatory, splenic, blood or bone disorders and for generating continuous directed against the receptor. A vector expressing a construct the extracellular cytokine binding domain of zcytor 10 cc is fused to the heavy chain of IgG gamma and the extracellular cytokine receptor subunit (an interlukin receptor subunit is fused to human zcytor 10 cr proposed to the heteromeric cytokine receptor subunit (an interlukin receptor subunit is fused to human server.)
                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand; binding; detection; modulation; recombinant cell; haematopolatic cell; lymph; immune system; blood; bone; inflammatory response; inflammation;
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 17; Page 120-121; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphoid and myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cytokine receptor mouse zcytor 10, useful for detecting ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200068381-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spleen;
                                                                                                                                                                                                                                                                                                                                                      interleukin receptor subunit) is fused to human kappa light
chain (See GENESEQ record AAA54474). The two sequences are fused
together using two primers (AAA54475, AAA54476).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stimulate proliferation or development of haematopoietic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-016096/02
                                     121
                                                                            159
                                                                                                                                                                                                                                        225;
                                                                                                               61
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                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g a nucleotide which encodes the zcytor 10 cytokine enables the production of recombinant cells expressing the
                                                                                                                                                                              EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                               NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
ISKAKGQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                     ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                            NWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                    330
                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0309861
                                                                                                                                                                                                                                                    97.2%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hammond
                                                                                                                                                                                                                                                        Score 1225; DB 22
Pred. No. 3.3e-90;
                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lok
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                    Gaps
                                                                          218
                                                                                                                  120
                                                                                                                                                         158
  278
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activities, and can be used in vaccines. (I) or an antibody binding (I) can be used for suppressing the immune system for reducing rejection of tissue or organ transplants and grafts and for treating T-cell specific leukaemias or lymphomas and autoimmune diseases including rheumatoid arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel disease and Crohn's disease. The antibodies can also be used for treatin immunologic renal diseases, glomerulonephritis, mesangloproliferative disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or vasculitis associated with lupus, polyarteritis, scleroderma, HIV-relate disease, amyloidosis and haemolytic uraemic syndrome. (I) and the antibodies can also be used for renal or urological neoplasms and multiple myelomas, asthma, bronchitis, emphysema and other chronic

for treating

HIV-related

and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic, antirheumatic, antiarthritic, neuroprotective, antiinflammatory,

present invention describes an isolated human zcytor19 protein (I).

antidiabetic, nephrotropic, dermatological, anti-HIV and natious carred activities, and can be used in vaccines. (I) or an antibody binding (I)

airway diseases. Human zcytor19 is located to chromosome 1, more specifically to chromosome 1p36.11. The present sequence represents a human IgG gamma 1 heavy chain protein, which is used in an exampl

the

present invention

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RESULT 12
ABB81641
Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis; mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis; secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma; haemolytic uraemic syndrome; renal neoplasm; urological neoplasm; emphysema; chronic airway disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus; autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV; diabetes mellitus; inflammatory bowel disease; Crohn's disease; ast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic; antiarthritic; antidiabetic; nephrotropic; de
                                                                                                                                                                                                                                                                  Example 7; Page 171-172; 200pp; English.
                                                                                                                                                                                                                                                                                            Novel Zcytor19 polypeptides and polynucleotides useful for stimulating immune responses in animals for producing antibodies, and for treating autoimmune diseases, leukemia and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2000;
07-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IgG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB81641 standard;
                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABQ73076
                                                                                                                                                                                                                                                                                                                                                                                 Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-2001; 2001WO-US44808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                        2002-527700/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zcytor19; cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma 1 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-253561P
2001US-267211P
                                                                                                                                                                                                                                                                                                                                                                                Xu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                        INC
                                                                                                                                                                                                                                                                                                                                                                                Novak JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor; immunosuppressive; cytostatic; tic; neuroprotective; antiinflammatory; c; dermatological; anti-HIV; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                 Whitmore
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RESULT 1:
AAE21960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                       THE INVENTION relates to a method for treating or preventing a mediated condition or a Th2 cell mediated condition in a mamma method comprising administering to the mammal a pharmaceutical composition of a fact to the mammal a pharmaceutical composition.
composition comprising a death domain containing receptor (DR6) agonist or antagonist. The method is useful for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. A DR6
                                                                                                                                                                                                                                                                                                                                                                                                                                   H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide; acquired immunedeficiency syndrome; AIDS; human immunodeficiency virus; HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective, adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;
                                                                                                                                           composition comprising
                                                                                                                                                                          Treating or
                                                                                                                                                                                                                                 Heuer
                                                                                                                                                                                                                                                             (ELIL ) LILLY & CO
                                                                                                                                                                                                                                                                                                                  30-APR-2001; 2001WO-US11735
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                                                                                                                                                                                                                                                                                                                                                                          WO200185209-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis; transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis; autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; therapy; death apoptosis; rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE21960 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                      or preventing T cell or Th2 cell mediated condition e or multiple sclerosis in mammal, comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKT
                                                                                                 Page 132-133; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain containing receptor (DR6).protein-related protein.
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97.0%;
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                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain containing receptor; DR6; receptor; anaemia; arthritis; eczema; asthma; psoriasis; pancreatitis;
                                                                                                                                             death
                                                                        a method for treating
                                                                                                                                                                                                                              Song
                                                                                                                                           domain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1225;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                              antibacterial.
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                                                                                                                                         DR6 agonist or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                             muscular; lymphoid; immune; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zcytor17; chromosome 5; 5q11; cytokine receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune infertility, Behoet's disease, autoimmune quartities, fibrosing lung disease, organ rejection after transplantation, thrombotic thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS) or a condition or symptom related to the above mentioned diseases in a mammal. An DR6 antagonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with inmunodeficiency, aberrant apoptosis, bacterial, viral or microbial infection, complications of infection, bundan immunodeficiency virus (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pyloriassociated ulceration.
                                                                                                                                                                                                                                                                                                                                                                                                                                            antiinflammatory; antiviral; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB05736 standard; Protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated ulceration, cytoprotection during cancer treatment, recuperation from chemotherapy, recuperation from irradiation therapy, or a condition or symptom related to the above mentioned diseases in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with aberrant apoptosis, graft-versus-host disease (GVHD), rheumatoid arthritis, ezzema, asthma, atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nsulin-dependent diabetes mellitus, cancer, multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Sinhes 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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97.0%;
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Pred. No. 3
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                                                                                                                                                                                                                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polynucleotide encoding a cytokine receptor zcytor17 which useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders -
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                                                                                                                                                           AAM47856;
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                                 transgenic
                                              human rhinovirus;
                                                                                              Human Ig-gammal heavy chain
                                                                                                                               22-FEB-2002
                                                                                                                                                                                           AAM47856 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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29-JUN-2000;
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                                           immunoadhesin; intercellular adhesion molecule;
rhinovirus; immunoglobulin heavy chain; J chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                       PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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2000US-214955P.
2001US-267963P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 187-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                            (first entry)
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97.0%;
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Pred. No. 3.3e-90;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      environment. Production is significantly less expensive in plants than animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 7; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoadhesin for treating human rhinovirus chimeric intercellular adhesion molecule-1, and secretory component in association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising
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                             PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                       ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                       NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                    EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                          EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
  PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Pred. No. 3.3e-90;
3; Mismatches 4
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US-10-207-655-240	US-10-207-655-148	US-10-207-655-15	US-10-207-655-344	US-09-875-338-5	US-10-077-023-135	US-10-077-023-133	US-10-077-023-5	US-09-948-429B-8	US-10-124-905-8	US-09-747-669-3	us-10-290-703-3	US-09-948-429B-12	US-09-948-429B-4	US-10-124-905-12	US-10-124-905-4	US-09-740-002-27	US-09-822-698A-26	US-09-875-338-17	US-10-077-023-17	US-09-256-156-1	US-10-150-475A-6	US-09-948-018-16	US-10-193-616-14	US-09-949-713-22	US-10-084-139-10	
Sequence 240, App	148,		Sequence 344, App	Sequence 5, Appli	135,	133	5	Sequence 8, Appli	8,	Sequence 3, Appli	Sequence 3, Appli	12,	Sequence 4, Appli	12	4	27,	N	Sequence 17, Appl	17	1,	Sequence 6, Appli	e 16,	Sequence 14, Appl	Ν	Sequence 10, Appl	

ALIGNMENTS

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Sequence 3, Application US/09847208

Publication No. US20030082190A1

GENERAL INFORMATION:
APPLICANT: SAXON, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IgE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67,002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-09-847-208-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3
LENGTH: 232
                                                                                                                                                                                                                                                                                                                                                               Query Match
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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Similarity 100.0%;
PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                   PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                            ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                            NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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Pred. No. 1.6e-88;
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CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-09-847-208-2
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US-09-847-208-2
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LENGTH: 569
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                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: IGUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGUS MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Saxon, Andrew APPLICANT: Zhang, Ke APPLICANT: Zhu, Daocheng
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                                                                                                                                                                    OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to OTHER INFORMATION: (IgE)
                                                                                                                                                                                                            ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                   TYPE: PRT
                                                                            Local Si
hes 232;
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                                                                                              Similarity
                 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                            100.0%;
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                                                                        Score 1260; DB 9;
Pred. No. 4.6e-88;
Mismatches 0;
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Pred. No. 2.4e-88;
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US-10-207-655-208
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Sequence 208, Applic Publication No. US20 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/250,198
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/996,357
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,302
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
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                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                 Application US/10207655 o. US20030118592A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     David I
                                                                                                                                                                                                                                                                                                                                                                                                          97.2%;
97.0%;
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Pred. No. 7.5e-86;
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CURRENT APPLICATION NUMBER: US/10/207,655

APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN
FILE REFERENCE: 390069.401C1

FUSION

CURRENT FILING DATE: 2002-07-25 NUMBER OF SEQ ID NOS: 426

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LENGTH: 247;
TYPE: PRT;
ORGANISM: Homo sapiens
US-09-996-357-13
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SEQ ID NO 208
LENGTH: 235
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                                                                                                                                                                   Query Match
Best Local Similarity
Matches .225; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/996,357
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,302
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/250,198
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/257,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE FILE REFERENCE; PPI-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Joyal, John L
APPLICANT: Gosselin, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gefter, Malcolm L
APPLICANT: Isreal, David I
                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 13
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ORGANISM: Artificial Sequence
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Local Similarity 97.08;
es 225; Conservation
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                                                  61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                  1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                 Application US/09996357
                                                                                                                                                                   Conservative
                                                                                                                                                                                 97.2%;
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Pred. No. 8e-86;
3; Mismatches
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CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
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; SEQ ID NO 6
rength: 251
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Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10152363A Publication No. US20030103986A1 GENERAL INFORMATION:
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APPLICANT: Xu, Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Grant, Francis, J.
APPLICANT: Grant, Francis, J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103
FILE REFERENCE: 00-103
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                      Query Match
  Best Local Similarity
                                                                                                                                                                                                               APPLICANT: Rixon, Mark W.
APPLICANT: Gross, Jane A.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion
FILE REFERENCE: 01-20
CURRENT APPLICATION NUMBER: US/10/152,363A
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                            TYPE: PRT
                                                                                     ORGANISM: Homo Sapiens
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les 225; Conser
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  97.2%;
97.0%;
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97.0%; Pred. No. 8.2e-86;
tive 3; Mismatches 4
Score 1225; DB 9; Pred. No. 8.2e-86;
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RESULT 10
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US-09-996-357-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/996,357
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,302
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/250,198
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEO ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-996-357-12
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 Sequence 14,
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Best Local Similarity
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LENGTH: 267
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APPLICANT: Isreal, David I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                     156
                                                                                                                                               121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
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                                                                                                                                                                                            NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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Application US/09822851B
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97.08;
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Pred. No. 8.8e-86;
3; Mismatches 4
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RESULT 11
US-10-119-637A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Liu, Yang
APPLICANT: Liu, Xingluo
APPLICANT: Zheng, Pan
APPLICANT: Bai, Xue-Fenc
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Best Local s
Matches 225
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                                                                                                                                                                                                                   SEQ ID NO 14
                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Methods of Blocking Tissue Destruction by FILE REFERENCE: 22727/04117
CURRENT APPLICATION NUMBER: US/10/119,637A
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/822,851
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/192,814
PRIOR APPLICATION NUMBER: 60/192,814
PRIOR FLING DATE: 2000-03-29
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LENGTH: 288
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                                                                                                                                                                                                                                          SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 16
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APPLICANT: Bai, Xue-Feng
TITLE OF INVENTION: Methods
FILE REFERENCE: 22727/04047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/822,851B
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
                                                                                                                                       TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liu, Yang
                                                                              LOCATION: (1)..(52)
OTHER INFORMATION: mouse
                                                                                                  NAME/KEY: DOMAIN LOCATION: (1)..(
    OTHER INFORMATION:
                      NAME/KEY: DOMAIN LOCATION: (53)...
                                                             FEATURE:
                                                                                                                                                                                                 LENGTH: 288
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225; Conserv
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                      . (55)
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sequence created by inventor; not from any
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97.0%;
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Pred. No. 9.6e-86;
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known organism
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US-10-047-542-20
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US-10-047-542-20
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; LOCATION: (56)..(288)
; OTHER INFORMATION: human IgG1
US-10-119-637A-14
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RESULT 13
US-09-995-898A-15
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SEQ ID NO 20
LENGTH: 330
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APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905,0004,CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT APPLICATION NUMBER: PCT/US01/13932
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR FILING DATE: 2001-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/10047542 Patent No. US20020168367A1
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                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                       181
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Similarity 97.0%;
25; Conservative
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                                                                                         PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                     PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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97.0%;
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Pred. No. 9.6e-86;
3; Mismatches 4;
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APPLICANT: Presnell, S
APPLICANT: Xu, Wenfen
APPLICANT: No. US2003
; ORGANISM: Homo sapiens
US-09-892-949-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR PRIOR ETLING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/267,211
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FACTOR
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LENGTH: 330
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                                                    SEQ ID NO 38
LENGTH: 330
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FILE REFERENCE: 00-42
CURRENT PAPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
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APPLICANT:
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                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2000-06-29
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                               PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
                                                                                               SOFTWARE: FastSEQ
                                        TYPE: PRT
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Local Similarity 97.0%;
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Pred. No. 1.1e-85;
3; Mismatches 4:
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NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-805-68
Search completed: July 15, Job time: 20.7984 secs
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US-10-269-805-68
Sequence 68, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
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Best Local Similarity 97.0
Matches 225; Conservative
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Best Local Similarity
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
                                          219
                                                                                                        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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97.0%;
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Pred. No. 1.1e-85;
3; Mismatches 4;
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Pred. No. 1.1e-85;
3; Mismatches 4;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 ,
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-458-516-13
US-08-457-101A-7
US-08-378-939-10
US-08-487-550-4
US-08-487-550-8
US-08-284-391B-33
US-09-218-590-33
US-09-218-593-22
US-08-887-352B-14
US-08-887-352B-16
US-08-887-352B-16
US-08-887-352B-16
US-08-887-352B-16
US-08-887-352B-16
                                                                                                                                                US-08-457-918-7

US-09-180-100-22

US-08-784-512-3

US-09-176-228-3

US-09-176-228-3

PCT-US95-03866-12

PCT-US95-03866-14

PCT-US95-03866-14

PCT-US96-10043-9
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US-09-178-869-2
US-09-180-100-11
US-08-236-311-7
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732.958 Million cell updates/sec
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17, Appl
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US-08-595-043A-50
; Sequence 50, Application US/08595043A
reach No. 5935824
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APPLICANT: SGARLATO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                    TYPE:
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                   61
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Result No.

1219	1219	1219	1219	1219	1219	1219	1219	1219	1219	1219	1219	1219	1219	1219	1219	1219	1219
96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	96.7	. 96.7
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PCT-US93-07832-22	US-08-146-206C-22	US-08-437-642B-22	US-07-934-373C-22	US-09-301-593-18	US-08-466-163B-8	US-08-466-151-8	US-09-234-340A-71	US-09-121-952A-71	US-09-026-985-71	US-09-027-449-71	US-09-296-005-18	US-09-296-005-16	US-09-296-005-14	US-09-054-255-2	US-09-282-505-2	US-09-109-207C-18	0S-09-109-20/C-16
Sequence 22,	Sequence 22,	Sequence 22,	Sequence 22,	Sequence 18,	Sequence 8,	Sequence 8,	Sequence 71,	Sequence 71,	Sequence 71,	Sequence 71,	Sequence 18,	Sequence 16,	Sequence 14,	Sequence 2,	Sequence 2,	Sequence 18,	Sequence 16,
•	, Appl	, Appl	, Appl		Appli	Appli	, Appl	•	, Appl	Appli	Appli	, Appl	, Appl				

ALIGNMENTS

PROTEIN EXPRESSION

SYSTEM

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Minimum

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on:

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US-08-595-043A-50
                                                                                                                                                  Query Match
Best Local Similarity
Matches 225; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 220 MONTGOMERY STREET, CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                            EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                amino acid
                                                                       EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                                                                                                                                                         397-8338
                                                                                                                                                97.2%; Score 1225; DB 2; 97.0%; Pred. No. 1.1e-116; tive 3; Mismatches 4;
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Length 360; Indels

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Gaps

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RESULT 2
US-09-178-869-2
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                                                       EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 360
                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09180100 Patent No. 6306395
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LENGTH: 331
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                                                                                                                                                                       APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207p
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2,
ORGANISM: Homo sapiens 09-180-100-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hickey, William F
APPLICANT: Hammang, Joseph P.
APPLICANT: Hammang, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/178,869B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tao, Weng
APPLICANT: Wong, Shou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                         TYPE: PRT
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97.0%;
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; Pred. No. 1.9e
3; Mismatches
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1.9e-116;
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US-08-236-311-7
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Best Local Similarity
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                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/9:
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/84
FILING DATE: 18-FEB-1992
                                                                                                                                                    REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/1 FILING DATE: 02-OCT-1987. ATTORNEY/AGENT INFORMATION: NAME: Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-MAY-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-SEP-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                  LENGTH: 3/1
TYDE: amino acid
                                                                                                             TELEFAX: 415/952-98
TELEX: 910/371-7168
                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
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                                                                                                                                      415/952-9881
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SYSTEM: PC-DOS/MS-DOS
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N: 435
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97.0%;
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Pred. No. 2.1e-116;
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US-08-457-918-7
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Best Local (
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                  NFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Capon, Danies J. APPLICANT: Gregory, Timothy J. TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                    FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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                                                                    REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-0CT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: C
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                                TELEPHONE: 415/225-82:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                       NAME: Kubinec, Jeffrey S. REGISTRATION NUMBER: 36,575
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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26-AUG-1992
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Pred. No. 2.2e-116;
3; Mismatches 4;
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                                  US-08-784-512-3
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Sequence 3, Application Patent No. 5872209
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Patent No. 6306395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKAMURA, NO. 630
APPLICANT: NAGATA, Shigekazu
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TYPE: PRT
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Pred No. 2.2e-116;
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GENERAL INFORMATION:

APPLICANT:

BARTNIK,

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                             Sequence 3, Application Patent No. 6180334 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 9610
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HUGHES, Clare TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1) TITLE OF INVENTION: and native aggrecan to study the proteolytic TITLE OF INVENTION: "Aggrecanase" in cell culture systems
APPLICANT:
                APPLICANT:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                              1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                        ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                  NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                             EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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TYPE: Floppy disk
                                                                                                                                                                                                    ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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Suite 500, 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 amino acids
EIDENMUELLER, Bernd
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
1..396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIDENMUELLER, BE
BUETTNER, Frank
CATERSON, Bruce
                BARTNIK,
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                       97.2%;
                Eckart
                                                            US/09176228
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Pred. No. 2.4e-116;
3; Mismatches 4;
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PCT-US95-03866-12

Sequence 12, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: Cytomed, Inc. (all statements)

CytoMed, Inc. (a

(all states JS only)

except US)

APPLICANT:

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS: LENGTH: 396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: EP 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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COMPUTER: II
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345 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 396
                              181
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                                                                                        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                   61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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F INVENTION: An artificial invention:
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                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
               PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                        NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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Suite 500, 3000 K Street, N.W.
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1..396
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97.0%;
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Pred. No. 2.4e-116;
3; Mismatches 4;
                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                Sequence 14, Application PC/TUS9503866 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acid
                                                           APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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APPLICATION NUMBER: US 0
FILING DATE: 28-MAR-1994
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                                CORRESPONDENCE ADDRESS
                                             NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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   STREET:
                  ADDRESSEE:
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                                                                                                                                                                                                                                             PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 424
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                                                                                                                                                                                                                                                                                                            NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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E: Fish & Neave
1251 Avenue of the Americas
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VENTION: STABILIZED DIMER OF KIT LIGAND AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States of America
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97.0%;
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Pred. No. 2.7e-116;
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PCT-US96-10043-11
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                                                                                                                                                             STREET:
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                                                                                                                                STATE:
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Sequence 11, Application PC/TUS9610043 GENERAL INFORMATION:
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Best Local Similarity
             COUNTY: 02210-2804
ZIP: 02210-2804
COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IBM PC compatible
CMEDIUM TYPEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Haley Jr, James F
REGISTRATION NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: UFILING DATE: 28-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                       225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                         Version #1.30
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RESULT 12
PCT-US96-10043-9
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Best Local !
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                                                                                                                                                ZIP: 02210-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION
                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6:
FILING DATE: 14-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: P-SELECTIN | TITLE OF INVENTION: AND METHODS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICATION NUMBER:
                                                                                             CLASSIFICATION:
                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                CITY: Boston
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TELEX: 200154
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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Similarity 97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       The General Hospital Corporation
VENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
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                                                                                                                                 PCT/US96/10043
                                                            US 60/000,213
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US-08-397-411-7; Sequence 7, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Weiner
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
ETLING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                   STREET: UNE TO CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Link, Brian
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Bispecific Antibody.
TITLE OF INVENTION: B-Cell Lymphoma and
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                              APPLICATION NUMBER: US/O FILING DATE: 01-MAR-1995
                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                           COMPUTER:
                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lech, Karen F. REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225;
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6129914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weiner, George
                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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97.0%;
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                                  30,223
                 011823-004901
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Pred. No. 2.8e-116;
""smatches 4;
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                                                                                                                                                                                                                        Version #1
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Best Local S
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                                             TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HU
TITLE OF INVENTION: GP
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CO, NAPPLICANT: TSO,
                                                                                             REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                             FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,2
                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Boloner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Market E
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
STRANDEDNESS:
                                                                                                                                                                                                                                                   CLASSIFICATION:
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                              ENGTH:
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225; Conserv
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              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: William M. Smith
One Market Plaza, Steuart Tower,
                            449 amino acids
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                                                                                                                                                                                                   NUMBER: US 08/059,159
03-MAY-1993
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97.0%;
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Pred. No. 2.9e-116;
3; Mismatches 4;
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US-08-157-101A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08157101A Patent No. 5808032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                  TELEX: 6714627 CUCH INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3711
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                    TYPE:
                                                                                                                                                                                       TELEPHONE: 202-00-
TELEPHONE: 202-822-0944
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 05-APR-1994
                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                      NAME: TITUS, MARLANA K REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: PILLSBURY, MADISON & SUTRO 1100 NEW YORK AVENUE, N.W.
                                                                                                                                  459 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATSUKURA, SHIGI
TSURUOKA, NOBUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KURIHARA, TATSUYA
MATSUKURA, SHIGEKAZU
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                                                               peptide
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97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 449;
               Length 459;
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Best Local Similarity

Score 1225; DB 1 Pred. No. 3e-116;

DB 1;

Matches	225; Conservative 3; Mismatches 4; Indels 0; Gaps	0;
Оy	1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVVDVSHEDPEVKF 60	ŏ
Db	228 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 287	187
Qy		120
Db	288 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT	347
Qy	121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180	.80
Db	348 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 407	07
Оy	181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232	
Db	408 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 459	
Search con	Search completed: July 15, 2003, 07:02:38	

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:52:29; Search time 18.5549 Seconds (without alignments) 1657.949 Million cell updates/sec

Perfect score: Sequence: US-09-847-208B-6 1707 1 FTPPTVKILQSSCDGGGHFP.....HEAASPSQTVQRAVSVNPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5 283224 seqs, 96134422 residues

Searched:

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:* pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	υī	4	ω	2	1	No.	Result
409	409.5	410	411.5	412	413	413.5	414	415	416	428	428.5	430.5	(L)	39.	439.5	55.	469	470	471	570	576	576		716	751	793	1644.5	1707	Score	
24.0	24.0		•	•	•	•	24.3	•	٠	٠		•	•	•	•	•	27.5	•	•	•	33.7	33.7	•	41.9		46.5	٠	0	Match L	% Query
592	343	391	470	328	453	457	444	328	326	328	454	476	328	455	455	549	504	433	572	115	243	227	423	548	388	429	426	428	Length D	
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\$25705	S25644	MHHUBT	S22080	147160	S37768	S03961	PC4436	147159	G2HU	147161	мннy	MHMSM	.147158	A24976	MHMS	S04845	S00390	S31436	B46529	E53116	PH1216	PH1215	EHMSS	S38864	EHMS	EHRT	I36948	ЕННО	ID	
. Ig mu chain	Ig mu chain	_	heavy	Ig gamma 2b	Ig mu chain	Ig mu chain	noclonal	gamma 2a	gamma-2	Ig gamma 3	mu cha		gamma 1	Ig mu chain	mu ch	heavy	gamma ch	upsilon	Y heavy		epsilon	epsilon	epsilon	epsilon	epsilon	epsilon	epsilon-	epsilon	Description	
shee		chain	chain pre	G)	C reg	C regi	antibod	chain	chain C	chain	C regi	C	chain c ·	C regi	C	ain pre	chain (cl	chain -		'n	chain C	5		chain C	'n	chain C	in	chain C		

A; Molecule type: protein A; Accession: A94418

45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	3 1	30
394	395.5	396	396.5	396.5	397	397.5	398	399	399	400.5	402	402.5	404	404.5	405.5
23.1	23.2	23.2	23.2	23.2	23.3	23.3	23.3	23.4	23.4	23.5	23.6	23.6	23.7	23.7	23.8
399	472	475	627	479	393	330	446	469	330	277	324	452	474	329	458
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G2MSAM	S31459	S01321	S14683	MHRBM	G1MSM	GHHU	S40295	S37483	G2MSA	I47162	G1MS	MHHU	S15590	G2GP	MHRB
Ig gamma-2a chain	Ig gamma-1 chain -	Ig gamma-2b chain	Ig mu chain precur	Ig mu chain C regi	Ig gamma-1 chain C	Ig gamma−1 chain C	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma 4 chain c	Ig gamma-1 chain C	Ig mu chain C regi	Ig heavy chain - h	Ig gamma-2 chain C	Ig mu chain C regi

ALIGNMENTS

<pre>in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp. A; Reference number: A94418 A; Accession: A94418</pre>
A;Residues: 1-358','L',360-428' <max> A;Cross-references: GB;J00222; NID:9184755 A;Note: this sequence difference may be due to polymorphism R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.</max>
A; Accession: A90824 A; Molecule type: DNA
A;Title: Duplication and deletion in the human immunoglobulin epsilon genes. A;Reference number: A90824; MUID:83001945; PMID:6288268
R.Max. E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P. Cell 29, 691-699, 1982
A; Residues: 1-428 < SEN> A; Residues: 1-428 < CBL: 1000000 CBL: 10000000 CBL: 10000000 CBL: 1000000000000000000000000000000000000
A; Accession: A93491
A; Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon A: Reference number: A93491: MUID:83168897: PMID:6300763
R;Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; S Nucleic Acids Res. 11, 719-726, 1983
A;Residues: 320-428 <zha> A;Cross-references: EMBL:X63693; GB:S38668; NID:q32987</zha>
A; Accession: PH1214 A; Molecule type: DNA
A; Reference number: PH1214; MUID:92308839; PMID:1613458
by alternative DW
A;Cross-references: GB:J00222; NID:g184755
A; Residues: 2-428 <ued></ued>
A; Accession: A23195
A;Title: Long terminal repeat-like elements tlank a numan immunoglobulin epsilon pseu A;Reference number: A23195; MUID:84207910; PMID:6327276
R.Ueda S.; Nakai S.; Nishida, Y.; Hisajima, H.; Honjo, T.
A; Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
A: Molecule type: DNA A: Regidings: 1-428 <flas< td=""></flas<>
A; Reference number: AZZ//1; MOID:84Z380Z3; FMID:0Z34I64 A; Accession: A2Z771
A; Title: The sequence of a human immunoglobulin epsilon heavy chain constant region g
R;Flanagan, J.G.; Rabbitts, T.H. EMBO J. 1, 655–660, 1982
C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116;
19 epsilon chain C region - human C:Species: Homo sapiens (man)
EHHU EHHU I
PECILO 1
ALIGNMENTS

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A,Cross-references: GDB:119335; OMIM:147180
A;Map position: 14932.33-14932.33
A;Introns: 1/1; 104/1; 211/1; 319/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog F;22-87/Domain: immunoglobulin homology <IM2>
E;128-195/Domain: immunoglobulin homology <IM2>
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C; Geneti
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A:Molecule type: mRNA
A:Residues: 320-428 <ZH2>
A:Experimental source: myeloma U266-derived cell line AF-10
A:Note: sequence extracted from NCBI backbone (NCBIN:141701, R:Hellman, L.
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R;Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994

A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin A;Reference number: A53116; MUID:94103254; PMID:8276835

A;Accession: A53116
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A; Title: Purification and characterization
A; Reference number: S02438; MUID:88083554;
A; Accession: S02438
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A;Accession: D46536
A;Status: preliminary; not compared with conceptual translation
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A; Residues: 401-428 <HE3>
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A;Residues: 382-391 (HE2>
A;Cross-references: GB:S55276; NID:g263168;
A;Experimental source: B cell myeloma U-266
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A; Residues: 1-40;68-114;427-428
A; Cross-references: GB:L00022; 1
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232-301/Domain: immunoglobulin homology <IM3>
338-407/Domain: immunoglobulin homology <IM4>
                                                                              14/Disulfide bonds: interchain (to light chain) #status predicted 15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted 21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status 121,209/Disulfide bonds: interchain (to heavy chain) #status predicted
Best Local Similarity
                        Query Match
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Ig epsilon-chain - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I36948...
R;Sakoyama, Y.; Hong, K.
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A; Residues: 1-426 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A; Title: Nucleotide sequences of immunoglobulin epsilon
A; Reference number: 136948; MUID:87147196; PMID:3103123
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HEAASPSQTVQRAVSVNPGK
                               GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
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97.2%;
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R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.;
Nucleic Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from ra
A;Reference number: A93442; MUID:83064537; PMID:6292865
A;Accession: A93442
                                                   RESULT 4
EHMS
If epsilon chain C region (version 1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A02144
C;Accession: A02144
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A93442; A90937; A02143
C;Accession: A93442; A90937; A02143
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A;Residues: 'N',169-307,'L',309-342 <KIN>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication: glycoprotein; heterotetramer; immunoglobulin
C;Keywords: duplication: glycoprotein; heterotetramer; immunoglobulin
E;19-80/Domain: immunoglobulin homology <IMl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A9093
A; Contents: myeloma IR162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain LOU/c/Wsl, immunocytoma IR R; Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr.,
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                    R; Liu, F.T.; Albrandt, K.; Sutcliffe, Proc. Natl. Acad. Sci. U.S.A. 79, 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A90937
  A; Title:
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Best Local
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  Cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                        VIHEALREPRKLERTISKSLG 418
                                                                                                                                                                                                                                                                                AVHEAASPSQTVQRAVSVNPG 319
                                                                                                                                                                                                                                                                                                                                                   NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSG--FFVFSRLEVTRAEWEQKDEFICR
                                                                                                                                                                                                                                                                                                                                                                                                             KDWIEGEGYQCRVDHPHFPKPIVRSITKAPGKRSAPEVYVFLPPE-EEEKDKRTLTCLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYENGTPKLTCLVLDL-ESEENITVTWVRERKKSIGSASQRSTKHHNATTSITSILPVDA
                                                                                                                                                                                                                                                                                                                             NFFPEDISVQWLQDSKLIPKSQHSTTTPLKYNGSNQRFFIFSRLEVTKALWTQTKQFTCR
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  and nucleotide
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  sequence
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Pred. No. 1.1e-51;
                        7852-7856,
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                        J.G.; Katz,
52-7856, 1982
  of.
mouse
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                                            D.H.
immunoglobulin
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-388 <LIU>
A;Cross-references: GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220
A;Cross-references: GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;1-44/Domain: immunoglobulin homology (fragment) <IMI>
F;81-149/Domain: immunoglobulin homology <IM2>
F;81-149/Domain: immunoglobulin homology <IM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;186-254/Domain: immunoglobulin homology <IM3>
F;290-361/Domain: immunoglobulin homology <IM4>
F;10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, Nove
A;Description: Combination of a defined
A;Reference number: $38864
A;Accession: $38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig epsilon chain C region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C;Accession: S38864
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                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin C r F;353-421/Domain: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-548 < KIP>
                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Kipp, B.; Becker, W.;
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                                                                                                   238 FPPKPKDVLTRSTIQLYCFIYGHILNDVSVSWLMDDREITDTLAQTVLIKEEGKLASTCS
                                                                                                                                                                                                               140;
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                                                 69 ELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPT
                                                                                                                                                                                                               Similarity 45.0
40; Conservative
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KLNITEQQWMSESTFTCKVTSQGVDYLAHTRRCPDHEPRGVITYLIPPSPLDLYQNGAPK 357
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                                                                                                                                                                                                                                        41.9%;
45.0%;
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Pred. No. 1.3e-48;
                                                                                                                                                                                                                                     Score 716; DB 2;
Pred. No. 8.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              November 1993
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F;115-183/Domain: immunoglobulin homology <IMM2>
F;220-288/Domain: immunoglobulin homology <IMM3>
F;325-396/Domain: immunoglobulin homology <IMM4>
F;325-396/Domain: immunoglobulin homology <IMM4>
F;23-75,122-181,227-286,332-394/Disulfide bonds: #status
F;43,84,167,239,262,417/Binding site: carbohydrate (Asn)
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A;Introns: 91/1; 199/1; 307/1
A;Introns: 91/1; 199/1; 307/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical lig C;Complex: An immunoglobulin heterotetramer subunits associate hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; 9lycoprotein; heterotetramer; immunoglobulin C;Keywords: duplication; 9lycoprotein; heterotetramer; immunoglobulin E;16-77/Domain: immunoglobulin homology <IMM1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-423 <ISH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358
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                                                                                                                                                                                                                                                                                                                                                                    72 LSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
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      KLEKTISTSLG 416
                                                                                                                                                                                                                                                                                                                                         TEQQWMSESTFTCRVTSQGVDYLAHTRRCPDHEPRGAITYLIPPSPLDLYQNGAPKLTC
                                                                                                                                                                         VVDRPDFPKPIVRSITLPQVSQRSAPEVYVFPPPE-EESEDKRTLTCLIQNFFPEDISVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQEGELASTQSELT 71
                                                                                     WLGDGKLISNSQHSTTTPLKSNGSNQGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPR
                                                                                                                               WLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQ 308
                                                                                                                                                                                                                                                          LVVDLESEK-NVNVTWNQEKKTSVSASQWYTKHHNNATTSITSILPVVAKDWIEGYGYQC
                                                                                                                                                                                                                                                                                    LVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQC 191
                                                                                                                                                                                                                                                                                                                                                                                                                               CDPNA-FHSTIQLYCFIYGHILNDVSVSWLMDDREITDTLAQTVLIKEEGKLASTCSKLN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRKLEKTISTS 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQWLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLEVTRAEWEQKDEFICRAVHEAASP
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                                                TVQRAVSVNPG 319
                                                                                                                                                                                                                RVTHPHLPRALMRSTTKTS-GPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQ 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin heterotetramer subunit consists of two identical light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQTVQRAVSVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTCLVVDLESEK-NVNVTWNQEKKTSVSASQWYTKHHNNATTSITSILPVVAKDWIEGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQWLGDGKLISNSQHSTTTPLKSNGSNRGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQK 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YQCIVDHPDFPKPIVRSITKTPGQRSAPEVYVFPPPE-EESEDKRTLTCLIQNFFPEDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.7%;
43.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 678.5; DB 1
Pred. No. 3.7e-43;
5; Mismatches 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PH1216
If epsilon chain C region form 3 - human (fragment)
N;Alternate names: Ig epsilon chain C region, membr
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Exp. Med. 176, 233-243, 1992
A;Title: Two unusual forms of human immunoglobulin E encoded A;Reference number: PH1214; MUID:92308839; PMID:1613458
A;Accession: PH1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig epsilon chain C region form 2 - human (fragment) .
;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change 21-Jan-2000
C;Accession: PH1215
R;Zhang, K.; Saxon, A.; Max, E.E.
  В
                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin A;Reference number: A53116; MUID:94103254; PMID:8276835 A;Accession: D53116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Exp. Med. 176, 233-243, 1992
A;Title: Two unusual forms of human immunoglobulin E encoded A;Reference number: PH1214; MUID:92308839; PMID:1613458
A;Accession: PH1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                    A; Introns: 108/1
                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-243 <ZH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X63693
R;Zhang, K.; Max, E.E.; Cheah, H.I
J. Biol. Chem. 269, 456-462, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-243 < ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Zhang, K.;
J. Exp. Med.
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A; Residues: 1-227 < ZHA>
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J. Exp. Med.
                                                                                                                                                                                                                                                                              A; Note: sequence
                                                                                                                                                                                                                                                                                                  A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local s
Matches 108
                                                                                                                                                              Superfamily: immunoglobulin C region; Keywords: alternative splicing; immunoglobulin homology
                                                                                                                           Query Match
                                                                                     Matches
                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K.; Saxon, A.; Max, E.E.
                                           212
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                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PH1216; D53116
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PRAAPEVYAFATPEWPGSRDKRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPG
                                                                                                                                                                                                            immunoglobulin C region; immunoglobulin
                                                                                                                                                                                                                                                                              extracted
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                                                                                                                                                                                                                                                                            myeloma U266-derived cell line AF-10 cted from NCBI backbone (NCBIN:141701,
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                                                                                                       100.0%;
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chain C region, membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H.K.;
                                                                               Score 576; DB Z; .; Pred. No. 8.3e-36; ...
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                                                                                                                                                                                          immunoglobulin
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                                                                                                                                                                    <MMI>
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                                                                                                                           Length 243,
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A;Cross-references: EMBL:X65219; NID:g62442; PIDN:CAA46322.1; A;Experimental source: spleen A;Note: sequence extracted from North
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig Y heavy chain (7.85) - duck
N;Alternate names: Ig gamma chain (7.85)
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change ;
C;Accession: B46529; S20759
R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins,
J. Immunol. 149, 2627-2633, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: E53116
                                                                               Qy
                                                                                                                              Db
                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                          A;Note: sequence extracted from NCBI backbone (NCBIP:116127) C;Superfamily: immunoglobulin C region; immunoglobulin homolC;Keywords: immunoglobulin C;Xeywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: A;Reference number: A46529; MUID:93017865; PMID:1401901 A;Accession: B46529
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B46529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: myeloma U266-derived cell line AF-10 A; Note: sequence extracted from NCBI backbone (NCBIN:141701, C; Superfamily: immunoglobulin C region; immunoglobulin homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig epsilon chain C region, secreted splice form (cl
C;Species: Homo sapiens (man)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994
C;Accession: E53116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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      δÔ
                                            В
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A; Residues: 1-572 < MAG>
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A; Residues: 1-115 <ZHA>
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                                                                                                                            TPPEVQVLHSSVCSTLG--DDSVELLCVITGFSPPPVEVEWLVDG--APAHLVATMTRPQ
                                                                                     GELAS ----TQSELTLSQKHWLSDRTYTCQVTY --QGHTFEDSTKKCADSNPRG----VSA
                                                                                                                                                                    TPPTVKILQSS-CDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
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                                            REAGSKTYMATSQTNVSREDWKAGKAFTCRVKHPATGGTAQGHARFCPGSGAQSCSPIQI
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    YLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT
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                                                                                                                                                                                                                              27.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                Score 471; DB 2;
Pred. No. 1.6e-27;
                                                                                                                                                                                                           Mismatches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig upsilon chain - axolotl (fragment)
C:Species: Ambystoma mexicanum (axolotl)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C:Accession: S31436
Ig gamma chain (clone 36) - chicken (fragment)
N;Alternate names: Ig nu chain
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000 *C;Accession: S00390
C;Accession: S00390
R;Parvari, R; Avivi, A.; Lentner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schechter, EMBO J. 7, 739-744, 1988
A;Title: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, comb:
A;Reference number: S00390; MUID:88283642; PMID:3135182
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S31436
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S00390
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A; Residues: 1-433 <FEL>
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)2; Conservative
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                                                                                                                                                                                                                                                                                                                KDEFICRAVHEAASPSQTVQRAVSVNPGK
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72; Mismatches
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A;Residues: 'LC',3-308,'H',310-549 <LIT>
A;Cross-references: EMBL:X15114; NID:g64799; PID:g763031
A;Cross-references: EMBL:X15114; NID:g64799; PID:g763031
C;Superfamily: immunoglobulin C region; immunoglobulin hc
C;Keywords: glycoprotein; heterotetramer; immunoglobulin
F;26-199/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                R:Litman, G.W. submitted to the EMBL Data Library, A:Reference number: S05695 A:Accession: S05695
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclectide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin A;Reference number: S04845; MUID:89345103; PMID:2503814
A;Accession: S04845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain precursor - African clawed frog (fragment) C;Species: Xenopus laevis (African clawed frog) C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change C;Accession: $04845; $05695 R;AmemJya, C.T.; Haire, R.N.; Litman, G.W.
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A; Residues: 1-549 <AME>
A; Cross-references: EMBL:X15114
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A; Molecule type: mRNA
A; Residues: 1-504 <PAR>
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108; Conserv
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                                                                                                                                            Similarity
LASTQSELTLSQKHWLSDRTYTCQVTY-QGHT-FEDSTKKCADSNPRGVSAYLSRPSPFD 120
                                                                                    PTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTAS-TTQEGE 62
                                                   PTVEILQGPCASS----KSVELLCLITGYAPSEIKVHWLLNGQVTNISPSNSKPCKEENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLIQNFMPEDISVQWLHNEVQLPDARHSTT----QPRKTKGSG----FFVFSRLEVTRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KWNGGTVFACMAVHEAL-PMRFSQRTLQKQAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLVRGFRPRDIEIRWLRDHRAVPATEFVTTAVLPEERTANGAGGDGDTFFVYSKMSVETA 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYSLSSRVNVSGTDWREGKSYSCRVRHPATNTVVEDHVKGCPDGAQSCSP--IQLYAIPP
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                                                                                                                         Conservative
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                                                                                                                                          26.7%;
33.0%;
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Pred. No. 1.9e
60; Mismatches
                                                                                                                                          Score 455.5; DB 2
Pred. No. 2.1e-26;
                                                                                                                                                                                                                                                                                                                                                         April
                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                           1989
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Gene 15, 33-42, 1981
A;Title: Sequence of the gene
A;Reference number: A26239; MC
A;Accession: A26239
                                                                                                                                                                                                                                                                             R;Kawakami, T.; Takahashi, N.; Honjo, T.

Nucleic Acids Res. 8, 3933-3945, 1980
A;Title: Complete nucleotide sequence of mouse immunoglobulin A;Reference number: A02166; MUID:81076590; PMID:6255422
A;Accession: A02166
                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 16-Aug-1996
C;Accession: A02166; A26239; A26240; B02039
A; Molecule type: DNA
A; Residues: 1-455 <GOL>
A; Note: the sequence was
                                                                                                                                         R;Goldberg, G.I.; Va
Gene 15, 33-42, 1981
                                                                                                                                                          A;Note: the sequence was determined from the germline R;Goldberg, G.I.; Vanin, E.F.; Zrolka, A.M.; Blattner,
                                                                                                                                                                                                                A; Cross-references: GB:J00443
                                                                                                                                                                                                                                   A; Residues: 1-455 <KAW>
                                                                                                                                                                                                                                                         A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDWENKKQFNCKVVHPDLPSPIEKSIQKSQDPGTEPTITLLPPSDDELRNDFISLICMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLVTKEAKVYCVISRMA-STDDLTVQWSRSDGKKALAFDSAPEKAYDGTFTVKSTLKISP 413
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  determined from the
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germline gene
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R;Auffray, C.; Rougeon, F. Gene 12, 77-86, 1980
A;Title: Nucleotide sequence of a cloned cDNA corresponding A;Reference number: A26240; MUID:81165562; PMID:6260591
A;Contents: TEPC183 ç secreted a

of.

A; Accession: A26240 chain

A; MoLecule type: mRNA A; MoLecule type: mRNA A; MoLecule type: mRNA A; Residues: 1-225, 'N', 227-257, 'S', 259-367, 'K', 369-455 <AUF> R; Kehry, M.; Sibley, C.; Fuhrman, J.; Schilling, J.; Hood, Proc. Natl. Acad. Sci. U.S.A. 76, 2932-2936, 1979 A; Reference number: A26241; MUID:79223904; PMID:111247 L.E

A;Contents: annotation; MOPC 104E
A;Norte: this sequence has been revised in reference A02039. Carbohydrate binding R;Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L. Biochemistry 21, 5415-5424, 1982 site

A; Title: Complete amino acid sequence of a A; Reference number: A02039; MUID:83075344; mouse mu chain: PMID:6816276 homology

heavy chain

A; Accession: B02039 A; Contents: MOPC 104E

C; Genetics: A; Molecule type: protein A; Residues: 1-77,'N',79-100,'Q',102-225,'N',227-257,'T',259-367,'K',369-455

A;Introns: 1/1; 106/1; 219/1; 325/1 C;Complex: An immunoglobulin hetero

F;129-201/Domain: F;239-307/Domain: F;346-417/Domain: C;Keywords: alternative splicing; duplication; glycoprotein; F;21-91/Domain: 1mmunoglobulin homology <IMM1> C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int c;Superfamily: immunoglobulin C region; immunoglobulin homology immunoglobulin homology <IMM2>
immunoglobulin homology <IMM3>
immunoglobulin homology <IMM4> heterotetramer; immunog

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F;436-455/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-89/Disulfide bonds: #status experimental
F;46,211,243;281,442/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;136-199,246-305,353-415/Disulfide bonds: #status predicted
F;216,454/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:X03690; NID:g52381; PIDN:CAA27326.1; PID:g52382 A;Experimental source: strain C57BL/6 A;Note: the authors translated the codon AAG for residue 65 as Leu C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin
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A;Title: Allotypic differences in murine mu-genes.
A;Reference number: A24976; MUID:86176735; PMID:3083402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          If mu chain C region (allele b) - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 05-Jun:1988 #sequence_revision 05-Jun:1988 #text_change 21-Jan-2000 C;Accession: A24976
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A; Residues: 1-455 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A24976
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Best Local S
Matches 106
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                                                117 SPEDLEIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                         172 GSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLKNVSSTCAASPSTDILTFTIPP
                                                                                                                                                                                                             112 PNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVCVEDWNNRKEFVCTVTHRDLPSPQKKFISKPNEVHKHPPAVYLLPPAREQLNLRESAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LASTQ----SELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
                                                                                                                                       LASTQ-----SELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETYTCVVGHEAL-PHLVTERTVDKSTGK 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFADIFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPEDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
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SFADIFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVA 290
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tive 57; Mismatches
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Search completed: July 15, 2003, 06:59:32 Job time: 19.5549 secs

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GCAM_MOUSE
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GCAM_MOUSE
GCB_RAT
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"A model of the Fc of immunoglobulin E.";
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EPC_RAT STANDARD; PRT; 4
PO1855;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig epsilon chain C region.
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Pfam; PP00047; ig; 4.
SMART; SMONATO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE=82174576; PubMed=6803238; Hellman L., Pettersson U., Bennich H.; "Characterization and molecular cloning of the mRI (epsilon) chain of rat immunoglobulin E."; Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
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InterPro; IPR003597;
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cloned cond probe for rat a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=LOU/C/WSL;
MEDLINE=83064537; PubMed=6292865;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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SM00407; IGC1; 1.
E; PS00290; IG_MHC; 3.
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GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                     TKPTVDLLHSSCDPNA-FHSTIQLYCFVYGHIQNDVSIHWLMDDRKIYETHAQNVLIKEE
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P06336; P01856;
21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence upda
15-JUL-1999 (Rel. 38, Last annotation up
Ig epsilon chain C region.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognat
NCBI_TaxID=10090;
                                                       InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; ig; 4.
SMART; SM00410; IG_like; 2.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunog
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  MEDLINE-84236092; PubMed-6329728; Ishida N., Ueda S., Hayashida N., Miyata T., Honjo T. Ishida N., Ueda S., Hayashida N., Miyata T., Honjo T. "The nucleotide sequence of the mouse immunoglobulin comparison with the human epsilon gene sequence."; EMBO J. 1:1117-1123(1982).
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EMBL;
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                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Liu F.-T., Albrandt K., Sutcliffe
"Cloning and nucleotide sequence
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Nucleic Acids
[2]
SEQUENCE FROM
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                  SEQUENCE FROM N.A.

MEDLINE=82051295; PubMed=6795090;

Goldberg G.I., Vanin E.F., Zrolka

"Sequence of the gene for the cons

Balb/c mouse immunoglobulin.";

Gene 15:33-42(1981).
                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=81076590; PubMed=6255422;
Kawakami T., Takahashi N., Honjo
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                                                                                                                                                          Rawakami T., Takahashi N., Honjo T.; "Complete nucleotide sequence of mouse immunoglobulin n comparison with other immunoglobulin heavy chain genes. Nucleic Acids Res. 8:3933-3945(1980).
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Biochemistry 21:5415-5424(1982).
-i- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF
THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
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Kehry M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., I
"Anino acid sequence of a mouse immunoglobulin mu chain
"Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
                                                                                      VARIANT
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Pfam; PF00047; 1g; 4.
SMART; SM00410; IG_like; 2.
SMART; SM00407; IGCl; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
NCBL_TaxID=10090;
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EMBL; V00821; CAA24202.1; PIR; A02167; MHMSM.
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MEDLINE-80222874; PubMed-6771020;
Porers J. Davis M., Calame
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                                                                                      ween the Swiss Institute of Bioinfo
European Bioinformatics Institute
                                                                                                                                                                                                          ms of immunoglobulin mu chain. 1 20:303-312(1980). ALTERNATIVE PRODUCTS: DURING
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                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; Ig; 4.
SMART; SM00410; IG_like; 2.
SMART; SM00407; IGcl; 2.
SMART; SM00407; IG_MHC; 3.
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Ol-JAN-1988 (Rel. 06, Created)
Ol-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat Ig mu chain C region.
Mesocricetus auratus (Golden hamster).
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                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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Rodentia;
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PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin_domain; Immunoglobulin_domain;
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                                             LILRESATVTCLVKGFSPADIFVQWLQRGQPLSQDKYVTSAPMREPQAPHLYFTHSVLTV
                                                                                          ----RTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSG--FFVFSRLEV
                                                                                                                                             NVCVEDWDSGKEFVCTVTHRDLPSPQKKFISK---PREMNKTPPAVY--
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x MEDLINE-95255298; PubMed-7737190; Stoppini M., Bellotti V., Negri A., "Characterization of the two unique immunoglobulins.";
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"The primary structure of a human IgG2 heavy chain:
evolutionary, and functional implications.";
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MEDIINE-83001943; PubMed=6811139;
MEDIANE-83001943; PubMed=6811139;
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                                                                                                                                                                                                                                                                                                      MEDLINE=80114419;
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"Comparison of the hinge-coding
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Query Match
Best Local
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Ig; 4
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
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"Nucleotide sequence of Suncus murinus immunoglobulin
comparison with mouse and human mu genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Insectivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suncus murinus (House shrew) (Musk shrew).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                      CARBOHYD
                                               CARBOHYD
                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9378;
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16-OCT-2001
                                                                                                                                                                                                                                                                                            HSSP; P01842;
                                                                                                                                                                                                                     Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-FEB-1991 (Rel. 17, 11-FEB-1991 (Rel. 17, 16-OCT-2001 (Rel. 40, 19 mu chain C region.
                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                               X13920; CAA32113.1; ALT_INIT.
Similarity
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                                                                                                                                                                                                                                                                                                                                         license agreement (See http://www.isb-sib.ch/announce/
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BY SIMILARITY.
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N-LINKED (GLCNAC...) (POTENTIA
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Matches 95
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20-MAR-1987 (Rel. 0
16-OCT-2001 (Rel. 4
Ig mu heavy chain d
                                                                                                                     DOMAIN
DOMAIN
SEQUENCE
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P04220;
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                                                                                                                                                                                                                                                                                                                                                                                   amino-acid sequence of the N-terminal 42 positions.", Hoppe-Seyler's Z. Physiol. Chem. 365:105-118(1984).
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                               SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                             Pfam; PF00047; ig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84184186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                          InterPro; IPR003006; InterPro; IPR003597;
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PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIEVSWLREGK----QVGSGVTTDEVE
                            PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
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                                                                                                                                                                                                                    PS00290; IG_MHC; 3.
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156
262
391
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40, Last annotation updat
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S., Mihaesco E.,
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; Ig_c1.
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Pred. No. 1.36
61; Mismatches
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pre-C-parT (NO V REGION HO
CH2.
CH3.
CH4.
W; 9100843AF0CF021A CRC64;
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15-JUN-2002
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                    PARTIAL SEQUENCE FROM N.A. MEDLINE-82059479; PubMed-6795593;
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                                                                                                                  "Complete amino acid sequence
immunoglobulin.";
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MEDLINE-81066716;
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"The primary structure of a monoclonal IgM-Immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain
type), subgroup H III. Architecture of the complete IgM-molecule.
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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                     ts T.H., Forster A., Milstein C.P.;
immunoglobulin heavy chain genes: evolut
celta and C gamma genes and associated
c Acids Res. 9:4509-4524(1981).
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"Cloning and partial nucleotide sequence of human immunoglobulin mu
chain cDNA from B cells and mouse-human hybridomas.";

Proc. Natl. Acad. Sci. U.S. A. 77:6027-6031(1980).

-!- MISCELLANEOUS: ALL 4 COMBINATIONS OF THE S/G & V/G POLYMORPHISMS
AT POSITIONS 192 AND 216 HAVE BEEN OBSERVED IN HUMAN MU CHAINS.
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"Complete sequence of a cloned cDNA encoding rabbit secreted mu-c
of VHa2 allotype: comparisons with VHa1 and membrane mu sequences
J. Immunol. 132:490-495(1984).

-1- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF
THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
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SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 3.
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MEDLINE=84088930; PubMed=6418803;
Bernstein K.E., Alexander C.B., Reddy
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MEDLINE=75038072; PubMed=4429665;

Tracey D.E., Cebra J.J.;

"Primary structure of the CH2 hom antibodies.";
                                                                                                                                                                                    Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guilimmunoglobulin-G(2). II. Amino acid sequence and hinge region cyanogen bromide fragments.
Biochemistry 10:9-17(1971).
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Submitted (APR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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MEDLINE=71058486; PubMed=5538616;
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Pfam; PF00047;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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P01842; 7FAB
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SM00407; iGc1; 2.
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nilarity 30.6%;
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      sequence update) annotation updat
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Pred. No. 2.8e-2 
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    THE TET SEARCH BREEF TO BE READED BREEF BR
                                                                                                                                                                                                                                                                                                                                                      EMBL; V00793; CAA24172.1; EMBL; V00793; CAA24173.1; EMBL; V00793; CAA24174.1; -EMBL; V00793; CAA24175.1; EMBL; V00795; CAA24176.1; -EMBL; V00795; GAA24176.1; -PIR; A02159; G1MS.
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                                                                                                                           Alternative NON_TER
                                                                                                                                                                                                           Pfam; PF00047; ig; 3. SMART; SM00407; IGc1;
                                                                                                                                                                                                                                                MGD; MGI:96446; Igh-4.
InterPro; IPR003006; I
InterPro; IPR003597; I
                                                                                                                                                                                                                                                                                                                 HSSP; P01842; 7FAB.
GlycoSuiteDB; P01868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The disulphide bridges of a mouse Biochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE (MYELOMA MEDLINE=78242288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=80012837; PubMed=113776; Rogers J., Clarke P., Salser W.; "Sequence analysis of cloned cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 70-322 FROM N.A. MEDLINE=80012837; PubMed=113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and complete nucleotide gamma 1 chain gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Honjo T., Obata M.,
Takahashi N., Mano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=80045036; Pu
Honjo T., Obata M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Svasti J., Milstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=73008889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 76-32
MEDLINE=80202559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy
                                                                                                                                                                      [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma-1 chain C r
s musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a 1 chain gene.";
18:559-568(1979).
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loma gammal chain.";
hem. 253:6068-6075(1978).
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PubMed=98524;
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Sciurognathi; Muridae;
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SEQUENCE FROM N.A.
MEDLINE-81223894; PubMed=6787604;
Ollo R., Auffray C., Morchamps C., R
Ollo R., Auffray C., Morchamps C., R
                                                                                                                                                                                                                                                                                                                                                                                   Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated
Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-2A chain C region, A allele.
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                                                                                                                                                            "The complete nucleotide sequence of mouse i and evolution of heavy chain genes: further sequence-mediated domain transfer."; Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria;
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MEDLINE-81076554; PubMed-6777755;
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SMART; SM00407; IG_l; 2.
PROSITE; PS00290; IG_MHC: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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MEDLINE-74175517; PubMed=4831970;
BOUTGOIS A., FOUGEGREAU M., ROCCA-Serra J.;

"Determination of the primary structure of a m
"Determination of the primary structure of the mununoglobulin:amino-acid sequence of the Fc for the evolution of immunoglobulin structure
for the evolution of immunoglobulin structure
for J. Biochem. 43:423-435(1974).
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"Determination of the primary structure of a mouse gamma immunoglobulin. Identification of the disulfide bridges.
Eur. J. Biochem. 30:452-462(1972).
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family.":
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                     ATPEWPGSRDKRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSR
                                            HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVL
                                                          PNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT
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SEQUENCE (MYELOMA PROTEIN NO.,)
MEDLINE=83289131; PubMed=6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann Of antibodies.
"Three-dimensional structure determination of antibodies."
"Three-dimensional immunoglobulin IgG1"
""" of crystallized monoclonal immunoglobulin IgG1"
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21-JUL-1986 (Rel. 01
16-OCT-2001 (Rel. 40
Ig gamma-1 chain C r
Dreker L., Schwarz J., Reichel W., nilscumman.

Preker L., Schwarz J., Reichel W., nilscumman.

Rule of antibody structure. The primary structure of a monoclone light immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                "The covalent structure of a human Intrachain disulfide bonds: "; Biochemistry 9:3188-3196(1970).
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"The rule of antibody structure. The primary structure monoclonal IgG1 immunoglobulin (myeloma protein Nie). I chymotryptic peptides of the H-chain, alignment of the peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human im
Nucleic Acids Res. 10:4071-4079(1982).
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z J., Reichel W.,
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Opossum IgE heavy

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/note= "Epitope in FG Loop" 210 218	. 206	note= "Epitope in DE Loop"	. 175	/note= "Epitope in BC loop"	.145	∕label≖ IgE heavy chain C3 domain	. 211	note= "Linker between domains C2 and C3"	. 111	/note= "Epitope including C2C3 linker"	. 114	/note= "IgE heavy chain C2 domain"	03	tion/Qualifiers			<pre>vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;</pre>	<pre>antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;</pre>	<pre>IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;</pre>	1 C2-C3-C4 domains		entry)			rotein; 323 AA.		

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                                                                                                                                                                                                                                                                                                                                                                              Sequence
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15-SEP-2000;
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                                                   NEMPEDISVQMLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                                                                                                                 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                      RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
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/note= "Linker between domains C3 and 216..317
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Pred. No. 1.1e-129;
; Mismatches 0;
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RESULT 2
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                        Query Match
Best Local :
                                                                                                                                                                                   presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains optimised for expression in a state of the present sequence represents the human is the sequence of the present sequence represents the human is the sequence of the present sequence represents the human is the sequence of the present sequence represents the human is the sequence of the present sequence represents the human is the sequence of the present sequence represents the human is the sequence of the present sequence of the pres
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antiasthmatic;
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DB; ABK51133.
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ological; antiinflammatory; immunoglobulin E; IgE;
allergic rhinitis; asthma; atopic dermatitis;
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anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
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The amino acid sequence of the Ec(epsilon) CH2'-CH4 fragment covering amino acids 226-547. The DNA sequence was isolated from a human myeloma 266BL cDNA library screened with a probe corresp. to the N-terminus of The The region encoding amino acids 218-547 was cloned into the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;
constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
histamine; anti-allergenic; vaccine; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fc(epsilon)-CH2'-CH4 protein-sequence.
                                                                                                                                                                                                                 Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has epitope(s) not present in native IgE, also derived antibodies for treating or preventing allergies, inflammatory immune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-1996
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                                                                                                                                          Claim 3;
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                                                                                                                                        Page 32-33; 44pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                     Panero MJM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           & VACCINS
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                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pWT211 under control of the tryptophan promoter. The resultant protein produced contains some non-Fc amino acids. These were removed by replacing their coding sequence with a bicistronic linker. The resultant construct encodes the Fc(epsilon) constant heavy region from amino acids 226-547. When it is expressed in E.coli, the protein produced is a non-glycosylated Fc(epsilon) fragment. Altering the pattern of glycosylated Fc(epsilon) induces a thus rendering the Fc fragment immunogenic and able to induce antibodies that recognise native IGE but do not form histamine-releasing complexes. The Fc fragments can be used in anti-allergenic vaccines to modulate the intensity of immune responses
                                                          Misc-difference
                                                                                           Misc-difference
                                                                                                                             Misc-difference
                                                                                                                                                              Misc-difference
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nilarity 100.
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172
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'note= "glycosylation
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                                                                                                                                                                                                                                          224-547) mutant sequence
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RESULT 6
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Protein;

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10-NOV-1995 AAR77241; AAR77241

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                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                       allergy.
                                                                                                                                                                                                                                                                                                  The sequence represents a mutant sequence of a human Ig chain raminfor acids: 224,54,70, anhich is of sufficient leng Fc-epsilon RI and/or Fc-epsilon FII per receptor sites cells. The protein is useful in the study and treatmen
                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 6;
                                                                                                                                                                                                                                                                                                                                                                Mutated glycosylated polypeptide(s) contg. useful to study and treat allergy.
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HEAASPSQTVQRAVSVNPGK
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                                     NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
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                                                                                                                                                                                                                                                                                                is useful in the study
                                                                                                                                                                                                                                                                                                                                               55pp; English.
                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sutton
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any AA
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                                                                                                                                                                                                                                                                                                                                                                                                                         BJ,
                                                                                                                                                                                                                             Score 1707; DB 16;
Pred. No. 1.1e-129;
; Mismatches 0;
325
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Best Local S
Matches 320
                                                                                                                                                                                                                                                            The sequence represents the wild-type sequence of a human IgE-Fichain (amino acids 224-547) which is of sufficient length to bif re-epsilon RI and/or Fc-epsilon FII IgE receptor sites on human cells. The sequence is preferably mutated (see AAR75225) to represent a protein encoding a protein where Cys225 is mutated, optionally together with Val224, Ser226 and Arg227. The protein is useful in the study and treatment of allergy.
                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 35-36;
                                                                                                                                                                                                                                                                                                                                                  Mutated glycosylated polypeptide(s) contg. useful to study and treat allergy.
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                      Gould
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                                                                                                                                                                                                                                              Sequence
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DB; AAQ91170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment;
                                                                                                                                                                                                                   Similarity
                                                                                                                                     NEMPEDIS VQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                             LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                      FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
               HEAASPSQTVQRAVSVNPGK
                                                                          LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                        HEAASPSQTVQRAVSVNPGK
                               NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
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                                                                                                                                                                                                           Conservative
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CH THERAPEUTICS
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172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiallergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (amino acids
                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                      Sutton BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "glycosylation
                                                                                                                                                                                                                                                                                                                               55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asn394
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                                                                                                                                                                                                          0;
                                                                                                                                                                                                         Score 1707; DB 16;
Pred. No. 1.1e-129;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       LTD.
               320
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224-547) wild-type sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Young
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                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                            human
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                                                                                                                                                                                                                                                                                               IgE-Fc
to bind
human
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Query Match
Best Local S
Matches 320
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                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-1998;
22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB03642 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hellman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RESI-) RESISTENTIA PHARM AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB03642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic polypeptides useful for preventing the harmful immunoglobulin {\tt E} in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-365342/31
                                            241
                                                                   192
                                                                                                                132
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301
                                                                                         181
                                                                                                                                                                                                                                                        320;
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                                                                                                                                                              72
                                                                                                                                                                                     61
                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin E; IgE; vaccination;
; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                    Similarity
                                                                                                              GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
HEAASPSQTVQRAVSVNPGK
                                  NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                          FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                       FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                    NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                                                                                                                                                       331
                                                                                                                                                                                                                                                          Conservative
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99US-0401636
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                                                                                                                                                                                                                                                                                                                                                                                                                                               50pp; English.
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                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constant
                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                    Score 1707; DB 21; Pred. No. 1.1e-129;
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                                                                                                                                                                                                                                                                                331;
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RESULT 8
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Best Local
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                         This fusion protein has a low toxicity for allergy induced by IgE. It can be allergic dermatosis, atopic dermatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fused protein for allergy treatment - comprising interleukin-2 N\text{-}\text{terminal} residues, a linker and human immunoglobulin E Fc
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1988-149211/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ikeyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-1987;
28-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAKEDA CHEMICAL IND
                                                                                                                                                                                                                                                                  Similarity
                                                                                                                      GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120
                 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                          FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEAASPSQTVQRAVSVNPGK 331
RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                               367
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p;
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                                                                                                                                                                                                                                                   Conservative
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86JP-0281871.
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37..367
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                                                                                                                                                                                                                                                                                                                                                                                                          English.
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                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor; fusion protein; asthma; dermatitis
                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                Score 1707;
Pred. No. 1
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                           and is useful in there used in the treatment or bronchial asthma.
                                                                                                                                                                                                                                            DB 9; 1
1.3e-129;
0;
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                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                         therapy
                                                                                                                                                                                                                                                                                  367;
                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                 Gaps
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AAU80283
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                        Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunogloi
                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                    06-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                   06-SEP-2001;
                                                                                                                                                                                                                                                                  14-MAR-2002.
                                                                                                                                                                                                                                                                                               WO200220038-A2
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                                                                                                                         Von
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IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
vaccine; anaphylaxis, allergic rhinitis; asthma; atopic dermatitis;
heavy chain C domain.
                                               (PHAR-) PHARMEXA AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IgE heavy chain C1-C2-C3-C4 domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU80283 standard; Protein;
2002-383033/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEMPEDISVQMLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
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                                                                      2000DK-0001326
2000US-232831P
                                                                                                           2001WO-DK00579
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                     Hoegen
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                                                                                                                                                                                                                                                                                               /note=
272..2
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244..2
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113..2
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                       P,
                                                                                                                                                                                                          "Linker
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                                                                                                                                                                                  "IgE heavy
                                                                                                                                                                                                                                                                                                                                                         "IgE heavy chain C3
                                                                                                                                                                                                                                                                                                                                                                                                       "Epitope including C2C3 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                IgE heavy chain C2
                       Voldborg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy
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                        Gautam
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immunoglobulin

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RESULT 10
AAM50940
ID AAM50
XX AAM50
XX 15-MA
DT 15-MA
XX 19E;
KW 17tic
KW antia
KW antii
KW vacci
XX VACCI
YX LOMAI
ET DOmai
FT DOmai
FT DOmai
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Best Local S
Matches 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C1-C2-C3-C4 domains used to create the
                                                                                                                                                        urticaria; anaphylactic antianaphylactic; immunc antianflammatory; dermat
                                                                                                                                                                                                                                                                                                                       AAM50940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epitopes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examples;
                                                                                                                                                                                                                                 Human IgE epsilon chain constant region
   WO200209751-A2
                                             Domain
                                                                        Domain
                                                                                                                   Homo sapiens
                                                                                                                                              vaccine;
                                                                                                                                                                                                                                                              15-MAY-2002
                                                                                                                                                          immunoglobulin E; antibody; human; allergy; asthma; eczema;
caria; anaphylactic shock; allergic rhinitis; conjunctivitis;
anaphylactic; immunosuppressive; antiallergic; antiasthmatic;
inflammatory; dermatological; vasotropic; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                              409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                             RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                                                                                                                                                                        HEAASPSQTVQRAVSVNPGK 320
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                                                                                                                                              therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative
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                                          /label= CH1
313..428
                                                                                    Location/Qualifiers
                              /label= CH4
                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151pp; English.
                                                                                                                                                                                                                                                                                                                         428
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129;
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constant region. The invention is based on the discovery that a CC polypeptide that includes the CH1 (i.e. constant domain 1 in the CH2 cyclain) and/or CH4 domain(s) of an IgE molecule, coupled to a CC carrier, can be used to induce in a mammal the production of antibodies that specifically bind to IgE of the mammal. Compositions are provided for inducing self-specific anti-IgE antibodies. These contain carriers foreign to the immunised mammal coupled to polypeptides containing fragments of the IgE molecule, coupled to polypeptides containing fragments of the IgE molecule, coupled to polypeptides containing fragments of the IgE molecule, coupled to polypeptides containing fragments of the IgE molecule, composition acids 1-110, 105, 5-105 or 5-95 of the present sequence, but not the CH3 domain. CH1 polypeptides have at least 95% identity to amino acids 133-428, 313-425, 317-428 or 317-425 of the present sequence. The compositions have at least 95% identity to amino acids 313-428, 313-425, 317-428 or 317-425 of the present sequence. The compositions reduce or eliminate the pool of free IgE in the mammal's serum. Alternatively, a polynucleotide encoding a fusion CC administered. The compositions and polynucleotides are used to inhibit or treat IgE-mediated disorders such as anaphylactic conditions, allergic rhinitis or conjunctivitis, an allergic reaction to compositions after the carrier of the composition of conditions and polynucleotides are used to condition allergic rhinitis or conjunctivitis, an allergic reaction to compositions and conditions and polynucleotides are used to condition allergic rhinitis or conjunctivitis, an allergic reaction to eccema or urticaria (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition for treating immunoglobulin (Ig) E-mediated disorder such as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises a polypeptide that includes CH1 and/or CH4 domains of IgE molecule coupled to a carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bachmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000; 2000US-221841P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Page 9; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RENNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Renner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WA.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nce is that of the human IgE epsilon cnain the invention is based on the discovery that
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comprises

Š Ş В QΥ В Ϋ́ В DЪ Дb δÃ Best Matches Local 289 181 229 121 169 109 320; 61 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD Similarity 100 20; Conservative RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 100.0%; 0; Score 1707; DB 23; Pred. No. 1.5e-129; Mismatches 0; Indels 0;

180

120 168

228

HEAASPSQTVQRAVSVNPGK

300

240 288

348

Query Match

.0%;

Length

Gaps

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409

HEAASPSQTVQRAVSVNPGK 428

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                                                                                                                                         Query Match
Best Local
                                                                         Matches
                                                                                                                                                                                   reduces its infectivity, competing with cell surface ICAM I for binding sites, interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty capsids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than in animal cell culture and production in plants is afer for human use, since plants are not known to harbor any animal viruses. The present the immunosity is that of a human immunoglobulin protein sequence, useful to
                                                                                                                                                                                                                                                                                                                                                                          reduces its infectivity, competing with cell surface ICAM-1 for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory component in association -
                                                                                                                                                                                                                                                                                                                                                                                                                            chimeric ICAM-1 molecule. The immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an immunoadhesin comprising:

(a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising rhinovirus receptor protein linked to at least a portion of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-2000; 2000US-200298P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Ig-E heavy chain constant region amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM47863 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PLAN-) PLANET BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-2001; 2001WO-US13932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          numan rhinovirus;
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DB; ABA05278.
       109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoadhesin;
                                                                                        Similarity
FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60
                                                                                                                                         428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 7; 138pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wycoff KL
                                                                      Conservative
                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin
                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intercellular adhesion molecule; ICAM-1;
unoglobulin heavy chain; J chain; HRV; common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                      0;
                                                                                    Score 1707; DB Pred. No. 1.5e-1
                                                                    Mismatches
                                                                                  DB 23;
.5e-129;
                                                                    Indels
                                                                                                  Length
                                                                    0
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and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9967293-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY79994 standard; Protein;
(non-anaphylactogenic) antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNBI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                            1; Page 66-68; 155pp; English.
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Best Local
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antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
heavy chain C domain; MIGIS.
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Domain
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                                                                                                                                                                                                                                                                                                             (first entry)
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104..111
                  /note=
216..31
                                     /note=
212..2
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210..21
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139..14
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                                                                                  /note=
                                                                                                    /note=
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                                                                                                                                                                    /note= "IgE heavy chain C2 domain"
100..114
                                                                                                                                                                                               Location/Qualifiers
                                                                                            167..175
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                                                                                                                                  . 211
                            "Linker between domains C3 andC4"
                                                               "Epitope
                                                                                 "Epitope
                                                                                                  "Epitope
                                                                                                                                        "Linker domain between C2 and C3 region"
                                                                                                                                                           "Epitope including C2C3 linker"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention.
          "IgE heavy chain C4 domain"
                                                                                                                      "IgE heavy chain C3
                                             "Epitope
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Pred. No. 3.3e-129;
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                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing immune response against autologous immunoglobulin E in animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunog
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15-SEP-2000;
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304
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               HEAASPSQTVQRAVSVNP
                                                                   NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                          RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                         RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                             LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                    NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
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2000US-232831P
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100.0%; Pr
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RESULT

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This invention relates to a novel method for inducing an immune respons, against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentiation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes
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                                                                                                           Inducing
                                                                                                                                                                                  06-SEP-2000;
15-SEP-2000;
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antiasthmatic; dermat
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                                                               Examples; Page 116-117; 151pp; English
                                                                                          lymphocyte
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by effecting simultaneous presentation of cytotoxic T
yte epitope an/or B-cell epitope derived from the immunoglobulin
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2000US-232831P
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321..422
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427..4:
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; MIGIS.
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                                                                                                                                                                                                                                                                 "MIGIS fragment"
                                                                                                                                                                                                                                                                                   "IgE heavy chain
                                                                                                                                                                                                                                                                                                     "Linker between domains C3 andC4"
                                                                                                                                                                                                                                                                                                                       "Epitope including C3C4 linker"
                                                                                                                                                                                                                                                                                                                                         "Epitope
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antiinflammatory; immunoglobulin E; IgE;
rhinitis; asthma; atopic dermatitis;
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RESULT 15
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C1-C2-C3-C4 domains fused to the MIGIS
                     Polypeptide having act from host transformed
                                                                                                                                                                                                                EP102634-A.
                                                                                                                    (TAKE )
                                                                                                                                           07-SEP-1982;
                                                                                                                                                                  03-SEP-1983;
                                                                                                                                                                                         14-MAR-1984.
                                                                                                                                                                                                                                        Homo sapiens
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                                                         1984-070437/12
DB; AAN40062.
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                                 having activity
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                                                                                                                    CHEMICAL
                                                                                                                                           82JP-0156285
                                                                                                                                                                   83EP-0108699
                                                                                                                                                                                                                                                              suppressor;
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                      recombinant
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                                 of human
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Pred. No. 1.2e-128;
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                                                                                                                                                                                                                                                              immunological
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Disclosure;

Fig

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English

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Search completed: July 15, 2003, 06:57:40 Job time: 39.6806 secs
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Best Local Similarity 99.4%;
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding IgE H-chain and frags. is claimed (AAN40062).

Transformant contg. the DNA is also new, esp. Escherichia coli IFO-
14284, -5 and -6. The transformant may be grown to produce a
polypeptide of immunological or biological activity equivalent to
that of the human IgE H chain. AAN40062 or frags. is pref. linked at a
site downstream from a promoter, e.g. rec A promoter (see AAN40064).
                                             414
                                                                                                      241 NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
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Pred. No. 2.5e-128;
0; Mismatches 2;
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430.5
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seg length: 2000000000
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1707
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 Listing first 45 summaries
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sp_mammal:*
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1833.165 Million cell updates/sec
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Q8VCX7
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11.3	16.3	17.3	17.3	17.3	17.3	17.3	17.3	17.4	17.5	17.7	17.8	17.8	17.9	17.9		19.0	19.4	9	9	9	9	0	0	1.	2	22.8	2	ω ·
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Q8WU38	Q905 44	Q8VCX4	Q91WR1	Q8VEA0	Q91X92	Q91WT1	Q91WT3	Q91XE1	Q91WP5	Q9DCD9	Q99KA4	Q91Z07	Q99LA6	Q8VCV5	Q99M22	Q9BRV0	Q96DK0	Q8WY24	Q96KX8	Q96K68	Q9UP60	Q9NPP6	Q96PQ8	Q9D8L4	Q8R3H6	Q91Z05	Q8TC63	Q8TC77
Q8wu38 homo sapien	Q90544 ginglymosto	Q8vcx4 mus musculu	Q91wr1 mus musculu	Q8vea0 mus musculu	Q91x92 mus musculu	Q91wt1 mus musculu	mus	Q91xe1 mus musculu	mus	Q9dcd9 mus musculu	mus	mus	mus	mus	2 mus	homo	homo	homo	homo	Q96k68 homo sapien	homo	homo	homo	Q9d8l4 mus musculu	Bun	5 mus	homo	Q8tc77 homo sapien

ALIGNMENTS

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RESULT 1
Q95M34
                                                          Query Match
Best Local Sim
Matches 106;
                                                                                                                               Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.;
Leibold W., Radbruch A.;
"Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
                                                                                                                                                                                                                                                                                                                                  Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region
                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=98383416; PubMed=9717671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q95M34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95M34
                                                                                   Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                    Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9796;
                                                            SEQUENCE
                                                                                                                 InterPro; IPR003006; Ig_MHC.
                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                          IGHC1.
                                                                                                                                                                                                                                                                                     W
               Similarity
                                                          337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
 26.3%; Score 448.5; DB 6; 31.3%; Pred. No. 1e-32; tive 62; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337
                                                                                                                                                                                                                                                                     databases
                             Length 337;
   Indels
   25;
 Gaps
   8
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δÃ

2 TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEG

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Query Match
Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 67.9 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 4.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2001) to the EMBL; BC018315; AAH18315.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8VCX7
                                                                                                                                                                                                                                                                                                                          PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003599;
InterPro; IPR003597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                 428
                                                                        369
                                                                                                                              309
                                                                                                                                                                                      249
                                                                                                                                                                                                                                             104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                       Similarity
                                                                                     LASTQ-----SELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
                                                                                                                                                                                                 PTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
              SVCVEDWNNRKEFVCTVTHRDLPSPQKKFISKPNEVHKHPPAVYLLPPAREQLNLRESAT
                                                                                                                             GSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLKNVSSTCAASPSTDILTFTIPP
                                          PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP--EWPGSRDKRT
                                                                     SFADIFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVA
                                                                                                                                                                                   PNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATPEWPGSRDKRTLACLIQNFMPEDISVQWIHNEVQLPDARHSTTQPRKTKGSGFFVFSR 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFYSLSSMYTVPASTWTSE-TYICNVVHAASNFKVDKRIEPIPDNHQKVCDMSKCPKCPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSVDRNRWQQGTTFTCGVMHEALHNHYT-QKNVSKNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTITKTKGRSQEPQVYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFNWYMDGVEVRTATTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAPKVFALAPGC -- GTTSDSTVALGCLVSGYFPEPVKVSW-NSGSLTSGVHTFPSVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRK 161
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            Ig_cl.
Ig_cl.
Ig_MHC.
                                                                                                                                                                                                                                                      25.2%;
                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                          Score 430.5;
Pred. No. 1e-3
56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata;
Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613
                                                                                                                                                                                                                                                       1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                          149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DSTKKCADSN--PR---
                                                                                                                                                                                                                                                                      613;
                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus.
                                                                                                                                                                                                                                          Gaps
              487
                                          234
                                                                                                 176
                                                                                                                                                                                   308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                RESULT
Q9BSZ1
B
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                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                   ₽
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                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                     ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
Q8R3V9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                Q9BSZ1;
01-JUN-2001 (TrEMBLrel. 17, Crea
01-JUN-2001 (TrEMBLrel. 17, Last
01-DEC-2001 (TrEMBLrel. 19, Last
Hypothetical 41.3 KDa protein.
Homo sapiens (Human).
                                                     Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                    Q9BSZ1
             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAR-2002) to the
EMBL; BC024405; AAH24405.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
TISSUE=LYMPH
                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08R3V9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8R3V9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                              4
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                                                                                                                                                                                                                                          442
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                                                                                                                                                                                                                                                                                                                                                                                                                                     113
                                                                                                                                                                                                                                                                                               384
                                                                                                                                                                                                                                                                                                                                                    324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                    292
                                                                                                                                                                                                                                                                                                                                                                                                            264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Similarity
97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                            TPPSVYPLAPG--SAAQTNSMVTLGCLVKGYFPEPVTVTW--NSGSLSSGVHTFPAVLQS
                                                                                                                                                                                                                                         GNTFTCSVLHEGLHNHHT-EKSLSHSPGK
                                                                                                                                                                                                                                                                                                                       KRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQ 291
                                                                                                                                                                                                                                                                                                                                                   SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD
                                                                                                                                                                                                                                                                                                                                                                               VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLYTLSSSVTVPSSTWPS-QTVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVF
                                                                                                                                                                                                                                                                   KDEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                             KVSLTCMITDFFPEDITVEWQWN--GQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEA
                                                                                                                                                                                                                                                                                                                                                                                                         IFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTKPREEQFNSTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELASTQSELTLSQKHWLSDRTYTCQVTYQGHTF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFICRAVHEAASPSQTVQRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTHSILTVTEEEWNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGS-GF-FVFSRLEVTRAEWEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETYTCVVGHEAL-PHLVTERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al protein.
469 AA; 5
                                                                                                           (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                   Chordata;
                                                       Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 414; DB 11;
Pred. No. 2.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                                                     Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534793F155D05457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314
                                                                                                                                                                    375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469
                                                                                                                                                                                                                                          469
                                                                   Vertebrata;
                                                       Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154;
                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - EDSTKKCADSNPRGVSAY
                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
Murinae; Mus
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469; 18;

Gaps

204

323 231

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20 밁 Ş 맑 Qγ 밁

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RESULT
Q99LC4
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     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2001) t
EMBL; BC004476; AAH044
HSSP; P01857; 1FC1.
Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 099LC4 PRELIMINARY: PRT; 4
099LC4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seque)
01-JUN-2002 (TrEMBLrel. 21, Last annot)
Similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                 EMBL; BC003435; AAI
HSSP; P01842; 7FAB
MGD; MGI:96446; Igi
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 375 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                 Strausberg
                                                                                                                            InterPro;
                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
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                                                                                        *2; TFA_
*2; TFA_
*36446; Igh-4.

*36446; Igh-4.

*36446; Igh-4.

*3646; Igh-4.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETYTCVVAHEAL - PNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                                                                                                  (FEB-2001) to the 33435; AAH03435.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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  _like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rođentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41314 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence
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                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 413; DB 4;
Pred. No. 2.1e-29;
3; Mismatches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B1A0A0998F473619 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
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Best Local S
Matches 96
Query Match
Best Local S
Matches 94
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (APF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-LYMPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                        SSP; P01825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
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  Conservative
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InterPro; 1:...

Pfam; PF00047; 1g; 5.

SMART; SM00409; IG; 2.

SMART; SM00407; IGc1; 4.

SMART; SM00406; IGv; 1.

SMART; SM00410; IG_like; 1.

SMART; SM00410; IG_like; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_3.

PROSITE; PS00290; IG_MHC; UDAFAD50A6375851 CRC64;

PROSITE; PS00290; IG_MHC; DAFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BQB8 PRELIMINARY; PRT; 597 AA.
Q9BQB8;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Unknown (protein for MGC:1905) (protein for MGC:1228).
                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JAN-2001) to the
EMBL; BC006180; AAH06180.1;
EMBL; BC001872; AAH01872.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPPSVYPLAPG---SAAQTNSMVTLGCLVKGYFPEPVTVTW---NSGSLSSGVHTFPAVLQS
                                                                                                                                                                                                            ; IPR003597; Ig_c1.
; IPR003600; Ig_like.
; IPR003006; Ig_MHC.
; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLYTLSSSVTVPSSTWPSE-TVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APR-2001)
                                                                                                                                                                                                                                                                                             IPR003599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG_MHC; UNKNOWN_1.
; 51007 MW; EAA674C6BBC30783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.2%;
                  24.2%;
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  63;
Score 413; DB
Pred. No. 3.9e
63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 413; DB 11;
Pred. No. 2.8e-29;
1; Mismatches 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GQPAENYKNTQPIMDTDGSYFIYSKLNVQKSNWEA
3; DB 4; 1
. 3.9e-29;
tches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463
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                                                                                                                                                                                                                                                                                                                                                                        databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                    Length
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                                        597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Indels

12;

Gaps

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RESULT
10 698
10 698
20 AC 098
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Submitted (CCT-2001) to the ENEMBL; BC015760; AAH15760.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 5.
PROSITE; PS00290; IG_MHC; UNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Hypothetical 65.0 kDa protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein SEQUENCE 597 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-B-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   096вв9
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           493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
     ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                 LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK
                                                                                                              PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE 62
                                                                                                                                                                                                                            SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                               LA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                 SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                           ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFICRAVHEAASPSQTVQRAVSVNPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETYTCVVAHEAL - PNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG_MHC; UNKNOWN_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 413; DB 4;
Pred. No. 3.9e-29;
3; Mismatches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
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RESULT
Q9R1A4
ID Q9
AC Q9
DT 01
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Q9BU10
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Best Local S
Matches 94
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00407; IG; 2.
SMART; SM00407; IGC1; 4.
SMART; SM00406; IGv; 1.
R SMART; SM00410; IG_like; 1.
R SMART; SM00410; IG_like; 1.
Q9R1A4;
Q9R1A4;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00
Hypothetical
SEQUENCE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U1-JUN-2UU1 (TrEMBLrel. 17, Creat 01-JUN-2001 (TrEMBLrel. 17, Last 01-DEC-2001 (TrEMBLrel. 19, Last Hypothetical 65.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC002963;
HSSP; P01825; 7F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-LYMPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                      LACLIQUEMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK
                                                                                                                                                                                                                                                    DEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                   SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE 62
                                                                                                                                                                                               ETYTCVVAHEAL - PNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                        TTCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETYTCVVAHEAL - PNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FEB-2001) to the 
02963; AAH02963.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al protein
597 AA;
(TrEMBLrel. 13,
                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7FAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig.
Ig_c1.
Ig_like.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.2%; Score 413; DB 4; 28.7%; Pred. No. 3.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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annotation update)
                                                       437
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; Homo.
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373

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RESULT
Q8WUX4
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Best Local S
Matches 97
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"Cloning of cDNAs encoding for anti-white pine blister rus:
antibody (Mab 7, its light and heavy chains) and construct
single chain antibody (scFV).";
Submitted (MAY 1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152372; AAD40243.1; -.
R HSSP; P01842; 7FAB.
RMGD; MGI:96446; Igh-4.
R InterPro; IPR003600; Ig_MHC.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003596; Ig_MHC.
                                                                                                                                                                                     O8WUX4 PRELIMINARY; PRT; 588 AA.

O8WUX4;
O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jalluna Jalluna (Mouse).

Mus musculus (Mouse).

"ravota; Metazoa; Chordata; "haria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
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01-JUN-2002
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                         SEQUENCE FROM
                                                                     NCBI_TaxID=9606;
                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                Hypothetical 64.4 kDa protein Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003596; Pfam; PF00047; ig; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT
: | | | | | | : | : | | : | | : | : | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPPSVYPLAPG--SAAQTNSMVTLGCLVKGYFPEPVTVTW--NSGSLSSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00290; IG_MHC; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVSLTCMITDEFPEDITVEWQWN--GQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLYTLSSSVTVPSSTWPSE-TVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELASTQSELTLSQKHWLSDRTYTCQVTYQGHTF-----EDSTKKCADSNPRGVSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEG
                                                                                                                                                                                                                                                                                                                                                                                                                           GNTFTCSVLHEGLHNHHT-EKNLSHSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 21, Last annotation updat y chain of Mab7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437
                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48142 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.1%; Score 411; DB 11; 29.5%; Pred. No. 3.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5C3A7BB3EE7D697C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.M., Misra S.;
white pine blister rust
chains) and construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      construction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monoclonal
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Q96EYO

ID Q96EYO

AC Q96EYO

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DT 01-MA

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Query Match
Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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Interpro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 4.
SMART; SM00406; IGV; 1.
PROSTIE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                                                  Pfam; PF00047; ig; 5.
SMART; SM00408; IGc2; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                      Submitted (JUL-2001) to the EMBL; BC011857; AAH11857.1; InterPro; IPR003598; Ig_c2. InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VI-MAK-2002 (TrEMBLrel. 20, Last annotation Unknown (protein for MGC:20337).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2001) to the EMBL; BC019235; AAH19235.1;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-B-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein SEQUENCE 588 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R
                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96EY0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96EY0
                                                                                         Immunoglobulin
SEQUENCE 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω
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                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETYTCVVAHEAL - PNRVTERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFICRAVHEAASPSQTVQRAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                           AA.
                                                                                                                 domain
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; Ig_c1.
; Ig_MHC.
; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; F
Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64438 MW;
                                                                                           67273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.7%;
                     23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                   Score 404; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last
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                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Pred. No. 2.5e-28;
Pred. No. 2.7
pred. No. 2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FC60DBAD82B39FD7 CRC64;
                                                                                           31214203FB8421E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
DB 4; 1
2.7e-28;
es 156;
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                                             613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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Conservative

62;

Indels

12;

Gaps

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RESULT 12
08WUK1
ID 08WUK
AC 08WUK
AC 08WUK
DT 01-MA
DT 01-JU
DE Hypot
OS Homo
OC Eukar
OC MARIMA
OT 01-GI
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RD SEQUE
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 92
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InterPro: IPR00306; Ig_MRC.
InterPro: IPR003596; Ig_v.
Pfam: PF00047; Ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 67.3 kDa protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 613 AA; 67296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; BC020240; AAH20240.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003597;
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       177
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                                                                                                                                                                                                                                                                                                                                                           l Similarity 28.6
92; Conservative
                                                                             SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                             LA-----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
  PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
                                                   SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                      ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                      PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                     PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETYTCVVAHEAL - PNRVTERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                23.7%;
                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                      Score 404; DB
Pred. No. 2.7e-
62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         60C7F5950671E315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613
                                                                                                                                                                                                                                                                                                                                                         DB 4; L
2.7e-28;
hes 156;
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 613;
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                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                   427
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RESULT 14
Q96AA6
ID Q96AA
AC Q96AA
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Q96A6

ID GA6

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Best Local S
Matches 92
  Q96AA6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissue=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
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                         PRELIMINARY;
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Q96GA6 PRELIMINARY; PRT; 614 AA. Q96GA6; Q96GA6; O1-DEC-2001 (TrEMBLrel. 19, Created) O1-DEC-2001 (TrEMBLrel. 19, Last sequence update) O1-MAR-2002 (TrEMBLrel. 20, Last annotation update) Unknown (protein for MGC:15420).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003006; Ig_
Pfam; PF00047; ig; 5.
SMART; SM00408; IGc2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; BC009851; AAH09851.1; -. InterPro; IPR000005; HTHArac. InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00041; HTH_ARAC_FAMILY_1; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain.
SEQUENCE 614 AA; 67
                                                DEFICRAVHEAASPSQTVQRAV
                                                                                                                                                   LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK
                                                                                                                                                                                                                                                                                                                                                                                                ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                              LA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
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                                                                                                ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                 SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                 PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
                                                                                                                                                                                                                                                                                                  SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
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ETYTCVVAHEAL-PNRVTERTV
                                                                                                                                                                                                                                                                                                                                               SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFICRAVHEAASPSQTVQRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETYTCVVAHEAL - PNRVTERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.7%; Score 404; DB 4; Length 614; 28.6%; Pred. No. 2.7e-28; Live 62; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55EF536E77AA9BBB CRC64;
                                                  314
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PRT;

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Q99L31
ID Q99L3
ID Q99L3
ID Q99L3
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DT 01-JU
DT 01
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Best Local :
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                                                                                                                                                                                                                                                                                                                         Q99L31 PRELIMINARY; PRT; 468 AA.
Q99L31;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
Mus musculus (Mouse).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017356; AAH17356.1; -.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003066; Ig_MHC.
Pfam; PF00047; ig; 5.
SMART; SM00408; IGC2; 1.
PROSITE; PS00290; IG_MC; UNKNOWN_3.
Hypothetical protein; Immunoglobulin domain.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 67.8 kDa protein.
Homo sapiens (Human)
                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                           Strausberg R.;
Submitted (FEB-2001)
EMBL; BC003878; AAH03
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=LYMPH;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                 InterPro;
                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETYTCVVAHEAL - PNRVTERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFICRAVHEAASPSQTVQRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LACLIQNEMPEDISVOWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                              IPR003599;
IPR003597;
IPR003600;
        IPR003006;
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                                                                                                                                      2001) to the AAH03878.1;
Ig.
Ig_cl.
Ig_like.
Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 404; DB 4; L-
bred. No. 2.7e-28;
bred. No. 156;
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                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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R Pfam; PF00047; ig; 3.

AR Pfam; PF00047; ig; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; IG_Like; 1.

DR SMART; SM00410; IG_MRC; UNKNOWN_1.

PROSITE; PS00290; IG_MRC; UNKNOWN_1.

PROSITE
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LRVEKKNWVERNSYSCSVVHEGLHNHHTT-KSFSRTPGK
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Search completed: July 15, Job time : 36.9679 secs 2003, 07:01:48

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Perfect score:
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Maximum Match 100%
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Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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US-10-047-542-60
US-09-949-375A-1
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US-10-214-524-37
US-10-207-655-334
US-09-949-375A-7
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US-09-949-375A-10
US-10-152-190-13
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1517.518 Million cell updates/sec
      Sequence 6, Appli
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Sequence 11, Appli
Sequence 31, Appli
Sequence 11, Appli
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Sequence 3, Appli	10 US-09-401-636-3	341	45.8	781	45
Sequence 3, Appli	US-10-176-	341		781	44
Sequence 27, Appl	9 US-10-214-524-27	426		788.5	43
Sequence 34, Appl	9 US-10-214-524-34	428		793	42
Sequence 2, Appli	10 US-09-401-636-2	340		793	41
Sequence 2, Appli	9 US-10-176-664-2	340		793	40
Sequence 33, Appl		567	47.1	804	39
35, A	US-10-214-524-3	563		823	38
Sequence 11, Appl	us-09-40	341	•	827	37
Sequence 11, Appl	9 US-10-176-664-11	341	48.4	827	36
30,	US-10-214-524-	569		906.5	35
Sequence 29, Appl	US-09-479-614-	496		949.5	34
2, 1	US-09-479-614-	496		949.5	ω
Sequence 14, Appl	_	431	55.6	949.5	32
Sequence 25, Appl	us-10-214-524-	496		955.5	31
Sequence 28, Appl	9 US-10-214-524-28	426		956.5	30
9, 1	US-	236		1011.5	29
Sequence 8, Appli	10 US-09-401-636-8	342	60.8	1038.5	28
8 A	9 US-10-176-664-8	342		1038.5	27
Sequence 2, Appli		222		1158	26
Sequence 6, Appli	US-09-809-715-	222		1158	25
14,	9 US-10-152-190-14	346		1364.5	24
-	us-10-152-	346		1435.5	23
•	US-10-152-1	348	Ė	1566.5	22
12,	9 US-10-152-190-12	347	92.5	1579	21
Sequence 26, Appl	9 US-10-214-524-26	426	9	1644.5	20

ALIGNMENTS

US-09-847-208-6

Sequence 6, Application US/09847208 Publication No. US20030082190A1

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                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CUGRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
LENGTH: 320
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                      Local
                                                                               121
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                                                                                                                               320;
                                                                                                                                                                                                  1 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                    Similarity
                                                                             FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                       RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
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                                                                                                       ; NAME/KEY: MISC_FEATURE : LOCATION: (196)..(206) ; OTHER INFORMATION: Epitope US-09-949-375A-2
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 323
                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09949375A Patent No. US20020172673A1
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                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 323
TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: DOMAIN LOCATION: (8)..(103) OTHER INFORMATION: Human
                                                                                                                                                                     NAME/KEY: MISC_FEATURE LOCATION: (167)...(175) OTHER INFORMATION: Epi
                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE LOCATION: (139)..(145) OTHER INFORMATION: Epi
                                                                                                                                                                                                                                                                         NAME/KEY: MISC_FEATURE LOCATION: (210)..(218) OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                                                                                                           LOCATION: (100)..(114)
OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC_FEATURE LOCATION: (100)..(114)
                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Linker
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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OTHER INFORMATION: Hum
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                                                                 Similarity
              FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60
 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 63
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US-09-949-375A-4
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LENGTH: 323
TYPE: PRT
ORGANISM: Artificial Sequence
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TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
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                                         ; OTHER INFORMATION: Synthetically US-10-176-664-1
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APPLICANT: KLYSNER, Steen et al.
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                  Sequence 1, Application US/1017664
Publication No. US20030031663A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
                                                                                                       SOFTWARE: FastSEQ for
SEQ ID NO 1
LENGTH: 331
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 Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/176,664
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                              PRIOR FILING DATE:
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                            TYPE: PRT ORGANISM: Artificial
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; OTHER INFORMATION: US-10-207-655-329
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US-10-207-655-329
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APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 329
LENGTH: 331
TYPE: PRT
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Pred. No. 8.6e+122;
); Mismatches 0;
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Sequence 5, Application US/09847208
Publication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhan, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT APPLICATION STEPLE COLOR-05-01
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NUMBER OF SEQ ID NOS: 177
SOFTWARE: FASTSEQ for Windows Version SEQ ID NO 5
LENGTH: 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09401636 Patent No. US20010038843A1
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SEQ ID NO 1
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CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
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ORGANISM: Artificial Sequence
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hes 320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                  Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60,
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Best Local
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CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 101
                                                                                                                                                                                                                                                                                                                           LENGTH: 42
TYPE: PRT
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hes 320;
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                                                                                                                 61 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
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Similarity 100.0%;
RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                 LFTRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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                                LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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Pred. No. 1.2e-121;
; Mismatches 0;
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RESULT 10
US-09-949-375A-1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09949375A Patent No. US20020172673A1
LOCATION: (113)..(208)
OTHER INFORMATION: Human
-09-949-375A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 42
TYPE: PRT
                                                                                                                                                    LOCATION: (317)..(320)
OTHER INFORMATION: Linker
                                                                                                                                                                                               NAME/KEY: MISC_FEATURE
LOCATION: (301)..(311)
OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE
LOCATION: (272)..(280)
OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE LOCATION: (315)..(323) OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE LOCATION: (205)..(219)
                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (209)..(216)
OTHER INFORMATION: Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: DOMAIN LOCATION: (11)...(116) OTHER INFORMATION: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: homo sapiens FEATURE:
                                   FEATURE:
NAME/KEY: DOMAIN
                                                                                                      LOCATION: (321)..(422)
OTHER INFORMATION: Human
                                                                                                                   NAME/KEY: DOMAIN LOCATION: (321).
                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Epitope
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NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Epitope including
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                                                           OTHER INFORMATION:
                                                                       NAME/KEY: DOMAIN
LOCATION: (217).
                                                                                            FEATURE:
                                                                                                                                                                           NAME/KEY: MISC_FEATURE
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APPLICANT: Bachmann,
APPLICANT: Renner, V
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                                                                                                                                                                                                                                                                                  TYPE:
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Query Match
Best Local Similarity
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                       HEAASPSQTVQRAVSVNPGK 320
                                                                                                    NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
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HEAASPSQTVQRAVSVNPGK 428
                                                                               NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
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Sequence 1, Application US Patent No. US20020146422A1 CURRENT APPLICATION NUMBER: US/09/916,230
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/221,841
PRIOR FILING DATE: 2000-07-28 APPLICANT: Renner, Wolfgang A. TITLE OF INVENTION: Compositions TITLE OF INVENTION: Antibodies a FILE REFERENCE: 1700.0140001 SOFTWARE: PatentIn version 3.0 NUMBER OF SEQ ID NOS: ORGANISM: Homo sapiens Application US/09916230 Antibodies and Uses Martin F. for Inducing Self-Specific Anti-IgE Thereof

LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ Score 1707; DB 10; Pred. No. 1.2e-121; ; Mismatches 0; 300 168 288 228

100.0%;

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Indels Length 428

0;

Gaps

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RESULT 13
US-10-047-542-45
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; OTHER INFORMATION: Fusion between hinge-CH2-CH3; OTHER INFORMATION: (IgE)
US-09-847-208-7
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US-09-847-208-7
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GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOI
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIPIAL
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
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CURRENT FILING DATE: 2001-05-01
NUMBER OF SEO ID NOS: 177
SOFTWARE: FASTSEO for Windows Version 4.0
SEO ID NO 7
LENGTH: 569
TYPE: PRT
                                                                                                                                              Sequence 45, Application US/10047542 Patent No. US20020168367A1
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Best Local Similarity
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TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Saxon, Andrew APPLICANT: Zhang, Ke APPLICANT: Zhu, Daochen
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Pred. No. 1.6e-121;
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Sequence 37, Application US/102145;
Publication No. US20030073142A1
GENERAL INFORMATION:
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa
APPLICANT: Chen, Zhong
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LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
US-10-047-542-45
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US-10-214-524-37
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; SEQ ID NO 37
; LENGTH: 574
; TYPE: PRT
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES FILE REFERENCE: IGE-00101.P.J.1
CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT FILING DATE: 2002-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
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PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
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                                 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
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Barankiewicz, Theresa
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                                                                                                  Conservative
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Pred. No. 1
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APPLICANT: Ledbetter, Jeffrey A.

APPLICANT: Ledbetter, Martha S.

TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 39069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 334
LENGTH: 592
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-10-207-655-334
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US-10-207-655-334
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Search completed: July 15, 2003, 07:17:19 Job time: 25.5495 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1707; DB 9; Length 592; Best Local Similarity 100.0%; Pred. No. 1.7e-121; Matches 320; Conservative 0; Mismatches 0; Indels 0
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Perfect score:
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Listing first 45 summaries
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Copyright (c) 1993 ~ 2003 Compug
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US-09-192-545-2
US-09-192-545-2
US-08-232-539D-56
US-08-433-105A-6
US-08-434-869A-6
US-08-466-163B-1
US-08-466-153B-1
US-08-466-1531-1
US-08-646-991-16
US-08-646-991-17
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US-08-336-583-2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN NUMBER OF SEQUENCES: 2
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ALIGNMENTS

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US-08-336-583-2
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336

FILING DATE: 09-NOV-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: CARTY, CHRISTINE:

NAME: CARTY, CHRISTINE:

NAME: OBON 1000 1000

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
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ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
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STREET: RAHWAY
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ZIP: 07065-0900
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                                      104 FIPPTVKLFHSSCNPVGDTHTTIQLLCLISGYVPGDMEVIWLVDGQKATNIFPYTAPGTK 163
60 EGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPF 119
                                                                                                                                         Similarity
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                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                single
                                                                                                                56.0%; score 956.5; DB 1; 56.2%; pred. No. 4.5e-84; tive 50; Mismatches 87;
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PCT-US95-13795-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FRIGTH: 426 amino acids
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GENERAL INFORMATION:
                                                                                                                                                                               Matches
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 594-6734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CHRISTING L. STREET: 126 E. LINCOLN AVENUE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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DLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVG 179
                                                                                                                               FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ 59
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                                                   EGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPF 119
                                                                                                       FIPPTVKLFHSSCNPVGDTHTTIQLLCLISGYVPGDMEVIWLVDGQKATNIFPYTAPGTK
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                                                                                                                                                                               Conservative
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ID NO: 2:
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56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               19211Y
                                                                                                                                                                                              Score 956.5; DB 5
Pred. No. 4.5e-84;
                                                                                                                                                                             Mismatches
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                             RESULT 4
US-08-232-539D-56
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US-09-192-545-2
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Sequence 56, Application US/08232539D Patent No. 5965709
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Matches
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EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Taya, Chóji
APPLICANT: Matsuoka, Kunie
TITLE OR INVENTION: Transgenic Animal Allergy Models and
FILE REFERENCE: 799P9570
CURRENT APPLICATION NUMBER: US/09/192,545
CURRENT FILING DATE: 1998-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Karasuyama, APPLICANT: Yonekawa, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 561
TYPE: PRT
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                                                                                                                                                                                                            251 WLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 CDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQEGELASTQSELT 71
                                                                                                                                                                                                                                                                                                                                                                                                                         72 LSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITC 131
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                                                                                                                                                                                                                                                                     RVTHPHLPRALMRSTTKTS-GPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQ
                                                                                                                                                                                                                                                                                                                     LVVDLESEK-NVNVTWNQEKKTSVSASQWYTKHHNNATTSITSILPVVAKDWIEGYGYQC
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Hiromichi
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Gaps

305

543

483 250 424 191 365 Methods for

GENERAL INFORMATION:

APPLICANT: Presta, Leonard APPLICANT: Jardieu, Paula NTITLE OF INVENTION: IGE Ant

IgE Antagonists

Paula M. 60

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CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES:

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RESULT 5
US-08-399-106A-6
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                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                     GENERAL INFORMATION:
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LENGTH: 113 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                APPLICANT: Presta, Leonard APPLICANT: Ridgway, John B.
                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/178583 FILING DATE: 07-JAN-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA
                                                                                                                      NUMBER OF SEQUENCES:
OMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San F
STATE: California
                                          STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                            101 CADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Amino Acid
              94080
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                                                                                                                                                                                    Presta, Leonard G.
                                                                                                                                                                                                   Carter, Paul J.
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                                                                                                                                                      A METHOD FOR
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100.0%; Pred. No. 3e-50;
tive 0; Mismatches
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                                                                                                                                                      MAKING HETEROMULTIMERIC
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APPLICATION NUMBER: US/08/399,106A FILING DATE: 01-Mar-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                  SOFTWARE: WinPatin (Generit CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
EILING DATE: 03-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/399
EILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,00
REFERENCE/DOCKET NUMBER: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acid
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                TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
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TYPE: Amino Acid
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TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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T: 460 Point San Bruno Blvd
South San Francisco
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415/952-9881
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                                                                                                                                                                                                                                                                                                                                             inch, 1.44 Mb floppy disk
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                                                                                                                                                                                                                                                                                    (Genentech)
                                                                                                                                                         08/399106
                                                                                                                                                                                                                                       US/08/433,105A
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US-08-434-869A-6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/3
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                Local Similarity
nes 110; Conserv
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                                                                                                                                                                               LENGTH: 110 Acid
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                                              211 GPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRK 270
271 TKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 320
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South San Francisco
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                               GPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRK 60
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                                                                                         34.4%; 5cc
100.0%; Pro
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A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
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                                                                                              Score 587; DB 2; 1
Pred. No. 2.7e-49;
0; Mismatches 0;
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Pred. No. 2.7e-49;
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RESULT 9
US-08-601-184-2
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US-08-037-579A-2
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Patent No. 5552537
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 398-3249
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                             APPLICANT: Zhang, Ke
APPLICANT: Max, Edward E
APPLICANT: Saxon, Andrew
TITLE OF INVENTION: IGE
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                 CORRESPONDENCE ADDRESS:
                                                                                NUMBER OF SEQUENCES:
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STREET: 4 Line CTTTY: San Francisco
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4 Embarcadero Cent
                             E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
4 Embarcadero Center, Suite 3400
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                                                                                                  ISOFORMS AND METHODS
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COMPUTER READABLE FORM:

941114187

COUNTRY:

California

MEDIUM TYPE: Floppy disk

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                                                                                                              ; TYPE: PRT; ORGANISM: Homo sapiens US-08-466-163B-1
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                                                                                                                                                          NUMBER
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                Matches
                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/466,163B CURRENT FILING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                            PRIOR FILING DATE: 1992-05-07
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 07/879,495
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APPLICATION NUMBER: US
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TELECOMMUNICATION INFORMATION:
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SOFTWARE: Patentin Pelantine
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                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/744,768
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GY: linear
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99.1%;
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                                             Score 566.5; DB 4;
Pred. No. 2.5e-47;
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APPLICANT: Jardieu et al. TITLE OF INVENTION: IMMUN

IMMUNOGLOBULIN VARIANTS 27

NUMBER OF SEQUENCES:

APPLICANT:

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US-08-464-025A-1
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US-08-232-539D-54
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Sequence 1, Applicati Patent No. 5994514 GENERAL INFORMATION:
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                                                                                                                                                                                                                                          Matches 105;
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CURRENT APPLICATION DATA:
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TELEPHONE: 650/225-1489
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APPLICATION NUMBER:
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TITLE OF INVENTION: IGE Antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/1
FTLING DATE: 07-JAN-1994
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                                                                                                                                                                                                                                                                                                                                         TYPE:
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                                                                                                                             168 GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP 212
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o. 5965709
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                                                                                                           61 GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP
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                                 Application US/08464025A
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SYSTEM: PC-DOS/MS-DOS
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/ 100.0%; Pr
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                                                                                                                                                                                                                                                          Score 556;
Pred. No.
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Best Local Similarity
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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                    CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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LENGTH: 119 amino acids
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
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MEDIUM TYPE: 3.5 inc
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                                                                          PRIOR APPLICATION DATA:
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CTTY: South San !
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                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DO: SOFTWARE: WinPatin (Genentech)
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CLASSIFICATION:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
                                                                                                               APPLICATION NUMBER: US/08/466,151 FILING DATE:
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                               CLASSIFICATION:
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SYSTEM: PC-DOS/MS-DOS
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N: 530
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Pred. No. 2.3e-43;
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INFORMATION FOR SEQ ID NO:
                REFERENCE/DOCKET NUMBER: 1 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KIMACHI, KA
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI,
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                 STREET: PO DOLL CITY: FALLS CHURCH
                                                   REGISTRATION NUMBER:
                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22040-0747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/1: FILING DATE: 26-JAN-1994
                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 118 amino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 DSNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRAS---GKPVNHS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 TRKEEKQR----NGTLTVTSTLÞVGTRDWIEGETYQCRVTHPHLÞRAL-MRSTTKTSGÞ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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Similarity 89.8%;
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                                                                                                                                                                                                                                                                                              VA
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                                                                                                                                                                                                                                                                                                                                    E: BIRCH, STEWART, KOLASCH AND BIRCH
PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIMACHI, KAZUHIKO
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EDA, YASUYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                        DOG-MOUSE HETEROHYBRIDOMA AND GENE FRAGMENT CODING FOR CONSTANT REGION OF CANINE
                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULINS
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                                                   32,181
                                                                                                                                          US/08/646,981
                                  1488-106
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Pred. No. 1.1e-41;
1; Mismatches 2;
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                                                                                                                                                                             Version #1.30
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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STRANDEDNESS: SIN
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                                                                                                                                                                                       FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/436,463
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 MLGGPSVFIFPPKPKDTLLIARTPEVTCVVVDLGPEDPEVQISWF-VDGKQMQTAKTQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 NPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHS-TRKE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GLYSLSSMYTVPSSRW-SSETFTCNVAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFE------DSTKKCADS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TAPSVFPLDPSC--GSTSGSTVALACLVSGYFPEPVTVSW-NSGSLTSGVHTFPSDLQSS
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TOKIYOSHI, Sachio
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N: 536
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                                                         KIMACHI-1
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Best Local S
Matches 108
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TYPE: a
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hes 108;
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  298
                                   284 VTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                   224 PEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLE
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                                                                                                                                                                                                                                                                107 --RGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEE 163
                                                                                                                                                                                                                                                                                                                         59 GLYSLSSMYTVPSSRWLSD-TFTCNVAHPPSNTKVDKTVRKTDHPPGPKPCDCPKCPPPE 117
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  amino acid
GY: linear
VDRSHWQRGNTYTCSVSHEALHSHHT-QKSLTQSPGK 333
                                                                             AQEELSRNKVSVTCLIKSFHPPDIAVEWEITGQPEPENNYRTTPPQLDSDGTYFVYSKLS
                                                                                                                                                           EQFNSTYRVVSVLPILHQDWLKGKEFKCKVNSKSLPSPIERTISKAKGQPHEPQVYVLPP
                                                                                                                                                                                                 KQRNGTLTVTSTLPVGTRDWLEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFAT
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Search completed: July 15, 2003, Job time: 14.8457 secs 07:02:41

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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Match Length DB
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Ig epsilon chain C	Ig gamma +2b chain Tα αamma heavy cha	Ig gamma-2 chain C	Iq qamma-2b chain	Iq qamma-2a chain	Ig epsilon chain C	Ig gamma-2b chain	Ig gamma-2a chain	Ig epsilon chain C	Ig gamma-2a chain			Ig gamma-2a chain		

ALIGNMENTS

EHHU RESULT

Ig epsilon chain C region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116;
R;Flanagan, J.G.; Rabbitts, T.H.
EMBO J. 1, 655-660, 1982
A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant region (A;Reference number: A22771; MUID:84236029; PMID:6234164
A;Recession: A22771
A;Molecula type: DNA
A;Residues: 1428 <FLA>
A;Residues

		 Ig gamma 1 chain c A;Title: Duplication and deletion in the human immunoglobulin epsilon genes. Ig gamma 3 chain c A;Reference number: A90824; MUID:83001945; PMID:6288268 Ig epsilon chain C A;Accession: A90824	epsilon chain C gamma-2 chain C	Ig gamma 2b chain A; McLecule type: mRNA Ig gamma 2a chain A; Residues: 1-428 <sen> If gamma 4 chain c A; Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:q185035</sen>		gamma-2 chain C	Ig gamma-3 chāin C	-	If gamma chain C r A; Residues: 320-428 < cZHA>	 Ty epsilon Claim Afficie: Two unusual folius of number limiting found in a encoded by afferhative KNA spiro	Ig epsilon chain C J. Exp. Med. 176, 233-243, 1992	R; Zhang, K.; Saxon, A.; Max, E.E.	A;ACCESION: A23195	A;Title: Long Terminal repear-like elements flank a numan immunoglobulin epsilon pseu A;Reference number: A23195; MUID:84207910; PMID:6327276	ng printed,		A) Residues: 1-426 (FLA)
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.	lymorphism Strom, H. Strom, B. Strom, B. Strom	munoglobulin epsilon genes. 288268	eder, P.	55; NID:q185035	300763	ing of human immunoglobulin epsilon	da, R.; Igarashi, K.; Kikuchi, M.;	32987		613458				a numan immunogiobulin epsilon pse 327276		55; NID:g185035 Honjo, T.	

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A;Cross-references: GB:S53497; NID:g263162; PIDN:AAB24855.1; A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backhonn (C):Genetics:
                                                                                                                                                                                                                             C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog E;22-87/Domain: immunoglobulin homology <IMI>
F;128-195/Domain: immunoglobulin homology <IM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.

J. Biol. Chem. 269, 456-462, 1994

A; Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts
A; Reference number: A53116; MUID:94103254; PMID:8276835
A; Accession: A53116
                                                                                           F;128-195/Domain: immunoglobulin homology <IM2>
F;333-301/Domain: immunoglobulin homology <IM3>
F;338-407/Domain: immunoglobulin homology <IM3>
F;338-407/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F;21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A46536; MUID:93122085; PMID:8419166 A; Accession: C46536
                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 14q32.33-14q32.33
A; Introns: 1/1; 104/1; 211/1; 319/1
                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:119335; ON A; Map position: 14q32.33-14q32.33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A;Title: Cloning and sequence determination of the gene for R:Reference number: A93933; MUID:83065234; PMID:6815656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 'GAWTL', 6, 'X', 8-16, 'B', 18-9
A; Experimental source: myeloma protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: IGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:S55276; NID:g263168; A;Experimental source: B cell myeloma U-266
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A; Residues: 382-391 <HE2>
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A; Residues: 382-426 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: myeloma U266-derived cell line AF-10 A; Note: sequence extracted from NCBI backbone (NCBIN:141701,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 320-428 <ZH2>
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A; Residues: 98-352
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A; Residues: 1-40; 68-114; 427-428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: D46536
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                                                ,209/Disulfide bonds: interchain (to heavy chain) #status predicted
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Similarity
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Score 1766;
Pred. No. 2
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DB 1;
.3e-102;
                     Length 428
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A; Accession: 136948
A; Status: preliminary;
                                Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A;Title: Nucleotide sequences of immunoglobulin epsilon
A;Reference number: 136948; MUID:87147196; PMID:3103123
                                                                   R;Sakoyama, Y.; Hong, K. Proc. Natl. Acad. Sci. U
                                                                                                  C; Accession:
                                                                                                                   C;Date:
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                                                                                                                g epsilon-chain - chimpanzee (fragment)
;Species: Pan troglodytes (chimpanzee)
;Date: 04-Oct-1996 *sequence_revision 0
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                                                    of chimpanzee
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Š 밁 Qy 밁 Qy В δÃ C; Superfamily: im F; 336-405/Domain: A; Introns: 103/1; 209/1; 317/1 C; Superfamily: immunoglobulin C A; Cross-references: A; Molecule type: DNA A; Residues: 1-426 <RES> Query Match
Best Local Similarity
Matches 338; Conserv Genetics: 305 105 245 186 129 62 ω STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY QRSLSLSPGKVEGGGGSGGGGS SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC REPOVYTLPPSRDELTKNOVSLT - - CLVKGFYPSDIAVEWESNGQPENNYKTTP - PVLDS --SRDFT-PTVKVLQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA RSPSLFPLTRCCKNIPSNATSVTLGCLAMGYFPEPVMVTWDA-GSLNGTTMTLPATTLTP Conservative immunoglobulin GB:M15398; 55.7**%**; 76.0**%**; NID:g176797; PIDN:AAA35416.1; 20; region; immunoglobulin homology <IMM> Score 1705.5; DB 2; Pred. No. 1.3e-98; 0; Mismatches 62; 2 Indels Length PID:g176798 426; 25; Gaps 61 364 161 304 244 104 8

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C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999 C;Accession: A9343; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R;Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982 A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93433; MUID:82274238; PMID:6287432 A;Accession: A93433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
GHHU
Ig gamma-1 chain C region - h
C:Species: Homo sapians (man)
                                          A; Note: this sequence has the Gl
R; Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol Chem.
A; Title: Die Primaerstruktur ein
                                                                                       A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E'
A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
                                                                                                                                                                                                          A; Note: this sequence has the Glm(3) marker, SR; RutLishauser, U.; Cunningham, B.A.; Bennett, Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gan A; Reference number: A90564; MUID:71064025; PMJ
                                                                                                                                                                                                                                                                                                                                                                        A:Residues: 88-113;235-330 <TAX>
A:Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human
A;Reference number: A90563; MUID:71064024;
A;Contents: myeloma protein Eu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Structure of human A;Reference number: S33887; A;Accession: S33887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z17370 R;Takahashi, N.; Ueda, S.; Obata, Cell 29, 671-679, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data A; Reference number: S33904 A; Accession: S36861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z17370
A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, A;Note: Lys-330 is removed after translation
R;Harris, L.J.
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A; Residues: 1-96, 'R', 98-135 <CUN>
                                                                                                                                                                                                                                                                                                                                                      A;Contents: myeloma protein A;Accession: B90563
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A; Residues: 88-113; 235-330
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A; Residues: 1-330 <EI
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      A91668;
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MUID:83001943;
      MUID:77070269;
                                              eines monoklonalen IgG1-Immunglobulins (Myelomprotein
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PMID:5530842
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PMID:5489771
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PMID:6811139
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                                                                    1976
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RESULT 4
$69339
Ig heavy chain V region precursor - human
C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-
C; Accession: $69339; $72664
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homm
Eur. J. Biochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chains in
A; Reference number: $69339; MUID: 95262687; PMI
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A;Cross-references: gDB:120085; OMIM:147100
A;Map position: 14q32.33·14q32.33
A;Map position: 124/1 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associa C;Superfamily: immunoglobulin cregion; immunoglobulin homology c;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IMID-F;37-206/Domain: immunoglobulin homology <IMSD-F;243-310/Domain: immunoglobulin homology <IMSD-F;243-310/Domain: immunoglobulin homology <IMSD-F;27-83,144-204,250-308/Disulfide bonds: #status experimental F;103/Disulfide bonds: interchain (to light chain) #status experimental F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental F;109/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglo A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
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A;Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A;Note: this sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330
A: Note: this sequence has the Glm(3) and Glm(non-1) markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: IGHG1
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A; Accession: B91668
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Best Local S
Matches 225
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PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                               PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                               Conservative
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Pred. No. 6.3e-69;
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pMID:4923144
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MUID:95262687; PMID:7744049

in human heavy-chain-deposition

disease

Preud'homme,

J.L.; Cogne, #text_change

19-Mar-1997

01-Dec

В

204

PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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R;Filpula, D.
submitted to the EMBL Data Library, February 1993
....rintion: Screeing method for protein-protein
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C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-255 <FIL>
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A:Residues: 1-140,'C',142-374 <KH2>
A:Cross-references: EMBL:X81695
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A; Accession: S72664
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A; Residues: 1-374 <KHA>
A; Cross-references: EMBL: X81695
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PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSSPGK
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                                                                  ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                               ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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96.1%;
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1.4e-68;
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A;Gene: GDB:IGHG3
A;Cross references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3
C;Superfamily: immunoglobulin C region; imm
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
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                                                                                                                                                                                  C; Keywords: immu F; 20-85/Domain:
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A;Title: Sequence of a human immunoglobulin gamma 3 heavy cha A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
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A; Residues: 1-234 (EHR)
C; Superfamily: immunoglobulin C region; immuno
C; Keywords: immunoglobulin
F; 48-117/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-377 < HUC>
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If gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision
                                                                                                                                                                                                                                                                                                                                   A;Cross-references:
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NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                    EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
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                                                                                                                                                                                  immunoglobulin homology <IMM>
                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                 GB:X03604;
                                                                                                                        37.2%;
89.7%;
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                                                                                                                                                                                                                                       145/3; 160/3; 270/3
                                                                                                                                                                                                                                                                                                                                 GB:M12958; NID:g33070; PIDN:CAA27268.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                         Score 1138; DB 2;
Pred. No. 1.9e-63;
1; Mismatches 13;
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PMID:2062315
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                                                                                                                                         Length
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Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A90219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser; E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1990
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
A;Reference number: A90442
A;Molecule type: protein
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication A;Reference number: A92219; MUID:77118561; PMID:402363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-3 chain C region, form LAT - human C;Species: Homo sapiens (man) C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text C;Accession: A60764 R;Huck, S.; Lefranc, G.; Lefranc, M.P. Immunogenetics 30, 250-257, 1989 A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A;Reference number: A60764; MUID:90007613; PMID:2571587 A;Accession: A60764
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G3HUWI
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C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-377 < HUC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP
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89.7%;
         chains,
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Pred. No. 2.5e-63;
         sequence
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       corresponding
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         residues
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         0f
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma hea A:Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Accession: A93906
A;Holecule type: DNA
A;Accession: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
                                                                                                                                                                                                                                                                                                                                           RESULT
G2HU
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PID: g6066056

heavy chain

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A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Molecules: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156
A; Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156
A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 59-125, 'EB',128-226,228-289 <WOL>
A;Residues: 59-125, 'EB',128-226,228-289 <WOL>
A;Note: this protein lacks most of the V region, all of the CH1 re
R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Fra
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports
A;Reference number: A39315; MUID:82247835; PMID:6808505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:IGHG3
A;Cross-references:
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A;Contents: heavy chain disease protein Zuc, partial sequence corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biophys. Res. Commun. 71, 907-914, 1976
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204;
                                                                                                                                                                                                                                                                                                                                                         59
                                                                                                                                                                                                                                   WYVDGVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                        EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                              NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
PMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG
                               PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPG
                                                                                                                                            ISKAKVQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                         EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
                                                                                                                   ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.7%;
88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1123; DB 1;
Pred. No. 1.1e-62;
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B.; Franklin,
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289
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Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
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                                                                                                             Qγ
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                                                                                                                                                                                                                                           QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgW, the subunits associate into kap hain disulfide bonds. In some cases, such as IgA and IgW, the subunits associate into kap hain disulfide bonds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Molecule type: protein
A:Residues: 1-19,'0','21-57,'z',59,'A',61-193,'D',195-325
A:Residues: 1-19,'0', 21-57,'z',59,'A',61-193,'D',195-325
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
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A;Residues: 238-275 <HOF>
R;Höfmann, T.; Parr, D.M.
R;Höfmann to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The amino acid sequences of the three heavy A;Reference number: A90752; MUID:80001357; PMID:11306 A;Contents: myeloma protein Zie A;Accession: A90752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene:
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A; Residues: 1-24, 'E', 26-57, 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Contents: myeloma
A; Accession: A92809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Hofmann, T.; Parr, D.M. Mol. Immunol. 16, 923-925,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: this sequence has since been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Milstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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121,
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                                                                                                                                                                                                             NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                        EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                         ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                      ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                          NWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT
                                                                                                                                                                                                                                                                                                         ERKCCVE----CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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88.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1107;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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that shown i
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PMID:113060
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PMID:118920
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in having
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C:Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #t C:Accession: A91749; A90220; A93228; A90245; A94416; R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G. Immunogenetics 18, 387-397, 1983
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DNA 1, 11-18, 1981
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C; Species: Homo
                                                                                                                                                                    Ig gamma chain C
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A; Residues: 1-327 <ELL>
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Best Local :
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Pred. No. 5.5e-61;
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                                                                #text_change
6; A02161
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F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status experim F;177/Binding site: carbohydrate (Asn) (covalent), #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hain disulfide bonds. In some cases, such as IgA and IgM, the subunits C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F; 20-65/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14432.33-14432.3
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
                                                               LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                     PQYYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFF 190
                                                                                                                                                                                                                                                                 NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE
                                                                                                                                                                                                                                                                                                NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
                                                                                                                                                                                                                                                                                                                                                                                                   LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
                                                                                                                                  PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
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16-Jul-1999

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A;Molecule type: protein
A;Residues: 132-143,'E','145-161 <FRU>
A;Residues: 132-143,'E','145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., ed., pp.109-127, Almqvist and Wiksell,
In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A;Reference number: A94416
A;Reference number: A94416
A;Reference number: A94416
A;Reference number: A94416
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',
A;Rote: this has the elf allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaphain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin bomology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;30-199/Domain: immunoglobulin homology <IM2>
F;336-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Nucleotide sequ
A;Reference number: A917
A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
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A; Title: Sequence studies of the Fd section of the heavy chain of ral A; Reference number: A90245; MUID: 70110015; PMID: 5461106
A; Accession: A90245
RESULT
I47160
Ig gamm
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A; Title: Heavy chain genes of rabbit IgG; isolation of a cDNA A; Reference number: A93928; MUID:83299917; PMID:6193512
A; Accession: A93928
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A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 < PRA>
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  gamma
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    chain
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                                                                                                                                                                                                              EWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQR
                                                                                                                                                                                                                                                                         KCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                                                                                                                                                                                                                                                                                                                                                      TCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPITHQDWLRGKEF
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1, 337-349, 1975
                                                                                                         SISRSPGK
                                                                                                                                              SLSLSPGK 232
                                                                                                                                                                                       EWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQK
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    region
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Pred. No. 1e-47;
  pig
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    (fragment)
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-328 < KAC>
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C;Superfamily: im
F;133-202/Domain:
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A;Status: preliminary; translated from GB/EA;Molecule type: mRNAA;Residues: 1-328 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Sus scrofa domestica (domest
C;Date: 21-Feb-1997 #sequence_revision
C;Accession: I47159
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R; Kacskovics, I.; S
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      밁
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Best Local Similarity
Matches 157; Conser
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Best Local
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                                                                                    165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE
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Sus scrofa domestica (domestic pig)
Feb-1997 #sequence_revision 21-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s, I.; Sun, J.; Butler, J.E.
153, 3565-3573, 1994
                                                                                                                                                                                                                                                                      Similarity
                         PQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS
                                                                                                                                                                   CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH 164
                                                                                                       NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE
    PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT
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region; immunoglobulin homology <IMM>

NID: g433123; PIDN: AAA52217.1;

PID:g433124

GB/EMBL/DDBJ

IgG identified PMID:7930579

from

the

cDNA sequences

of f

#text_change

21-Jan-2000

32;

Score 868.5; DB 2 Pred. No. 8.4e-47; 2; Mismatches 32

32;

Indels

Ψ

Gaps

284

224 130 2

Length

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A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Sus scrofa domestica (domestic pig); Species: 21-Feb-1997 #sequence_revision 21-Feb-1997
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                   NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
                                                                                                                                                                                                                                                                      CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                               PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
                                                                                                                                           TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE
                                                                                                                                                                                                                                 CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH
                                                         PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sun, J.; Butler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: U03780; NID: g433125; PIDN: AAA52218.1;
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2; Mismatches
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No. 8.4e-47;
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PMID:7930579
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A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 *sequence_revision 21-Feb-1997 *text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147162
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A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.3%; Score 865; DB 2; Length 277; Best Local Similarity 69.0%; Pred. No. 1.1e-46; Matches 158; Conservative 32; Mismatches 35; Indels
                                                                      184 DSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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P01857;
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                                                                          "The covalent structure of a hu Intrachain disulfide bonds."; Biochemistry 9:3188-3196(1970).
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Dreker L., Schwarz
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RATISHAUSER U., Cunningham B.A.,
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77070269; PubMed=826475;
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Biochemistry 20:2361-2370(1981).
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                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; ig; 3.
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PIR; !
PDB; 1
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I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE 35,116,198,269 & 272.
I- MISCELLANEOUS: EU ALSO DIFFERS IN THE 155, 166, 177, 195, 198, 269, AND 277
                                                                                                                                                                                                                                                                                                                                                           send
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A02146; GHHU.

1FC1; 15-JUL-92.

1FC2; 15-JUL-92.

EW; HGNC:5525; IGHG1.
                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             RESIDUES 198,267&272
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MISCELLANEOUS:
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SM00410; iG_like; 1.
SM00407; iGc1; 2.
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PubMed=7236608;
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K -> R (IN G1M(3) MARKER).

/FTId-VAR_003886.

D -> E (IN G1M(NON-1) MARKER).

/FTId-VAR_003887.

L -> M (IN G1M(NON-1) MARKER).

/FTId-VAR_00388.
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REVISIONS TO 12-97 (PROTEIN WIS).
MEDLINE-77118561; PubMed-402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of humar
quadruplication of a 15-amino acid residue basic
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Eukaryota; Metazoa;
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SEQUENCE (DISEASE PROTEIN WIS).

MEDLLINE-81021548; PubMed=6774747;

Frangione B., Rosenwasser E., Prelli F., Franklin E.

"Primary structure of human gamma 3 immunoglobulin c
gamma 3 heavy-chain disease protein Wis.";

Biochemistry 19:4304-4308(1980).
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Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

Proc. Natl. Proc. Proc. Natl. Proc. Proc. Natl. Proc. Proc. Natl. Proc. Proc. Proc. Natl. Proc. 
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[3]
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HSSP; P01857; 1FC1.
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GAMMA-3 HEAVY CHAINS.

GAMMA-3 HEAVY CHAINS.

GAMMA-3 HEAVY CHAINS.

MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUECLASS.

MISCELLABOOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
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147120; -.
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Heavy chain disease in man: cDNA sequence supports partial
     domain;
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                                                Takahashi N., Ueda S., Obata M., N:
"Structure of human immunoglobulin
evolution of a gene family.";
Cell 29:671-679(1982).
                                                                                                                                                             "Linkage and sequence homology of two human immunoglobulin "Linkage and sequence homology of two human immunoglobulin
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                 TISSUE=Fetal liver;
MEDLINE=83001943; PubMed=6811139;
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16-OCT-2001 (Rel. 40, Last annotation
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MEDLINE=84235992; TISSUE-Fetal

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InterPro; IPR003597; Ig_like.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
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"The amino acid sequences of the three he
domains of a human IgG2 myeloma protein.
Can. J. Biochem. 57:758-767(1979).
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"The primary structure of a human 1962 hea
evolutionary, and functional implications.
J. Immunol. 125:1048-1054(1980).
                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-72033500; PubMed-4940472;
Milstein C., Frangione B.;
"Disulphide bridges of the heavy chain
Biochem. J. 121:217-225(1971).
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MEDLINE=80114419; PubMed=118920;
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,77148; G2HU.
                                                                                                                                                                                                                                                               A02148; G2HU.
; P01857; 1FC1.
w; HGNC:5526; IGHG2.
                                                                                                                                                                                                                                        147110;
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                                           PS00290; IG_MHC; 2.
obulin domain; Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                        AAB59393.1;
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use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-sib.ch)
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Homo sapiens (Human).
Homo sapiens (Human).
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MEDLINE=83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin DNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                   constant region of a gamma 4 chain."; Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                  SEQUENCE OF 1-30 AND 81-326.
MEDLINE-70207560; PubMed-4192699;
Pink J.R.L. Buttery S.H. de Vries G.M.,
"Human immunoglobulin subclasses. Partial
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                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a deep the Swiss Institute of Bioinformatics and the EMBL
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      SEQUENCE OF 1-128.
MEDLINE-76135469; Puratt D.M., Mole L.F.
"Sequence studies or
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                                                                    SEQUENCE FROM N.A. MEDLINE=84030930; PubMed=6 Bernstein K.E., Alexander
                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006;
                                             mmunogenetics
                                                             Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                         Local 201;
                                                                                                                                    gamma chain
                                                     haplotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; K01316; AAB59394.1; ALT_INIT
A02150; G4HU.
                                                                                                                                                                                                                                                                   131
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SM00407; IGC1; 2.
E; PS00290; IG_MHC; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:5528;
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                              CPPCPÄPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                           LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE
                                                                                                                                                                                                                  LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
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                                                                                                                                                                                                                                                                                         NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE
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G
                                             18:387-397(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain;
                                                                                                                                                                            STANDARD;
                                                          PubMed=6313520;
"Trander C.B., Mage R
s on the constant region of different allotype.";
                                                                                                                                    region
               PubMed=1243651;
L.E.;
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90.5%;
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                                                                                                                                           sequence update)
annotation update)
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Pred. No. 1.4e
1; Mismatches
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CH2.
CH3.
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INTERCHAIN
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                                                            R.G.;
heavy
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                                                              chain
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Best Local
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Gamma globulins, Nobel symp Stockholm (1967).
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MEDLINE-83299917; PubMed=6193512;

MATCHES C.L., Moore K.W., Steinmetz M., Hood L., Knigh

"Heavy chain genes of rabbit IgG: isolation of a cDNA
heavy Chain and identification of two genomic C gamma
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                          SMART; SM00407;
PROSITE; PS0029
                                                                                                                                                                                                                                                                                                                     PIR; A02161; GHRB.
HSSP; P01857; 1FC1
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                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       modified and this statement
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Hill R.L., Lebovitz H.E., Fellow
                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                    InterPro; IPR003597;
                                                                                                                                                                                                                                                                                                                                                                 entities requires a
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"Sequence studies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin
                                                                                      Match
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104-THR, AND THE E14 MARKER, 1
MARKERS AND REF.5 THE E15 MARK
                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss institute of Bioinformatics and the European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
136
                                                                      160;
                 45
                                  76
                                                                             Similarity
٦.
                                  QPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                           PS00290;
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173
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                                                                     34;
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                                                                   Score 883; DB 1;
Pred. No. 7.6e-54
4; Mismatches 3
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A (IN E15 MARKER)

E (IN REF. 2).

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VPV (IN REF. 3).

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<sup>3</sup> AND 4
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 Query Match
                                                                                                                InterPro; IPR003006; Ig_MHC.
InterPro; IPR003397; Ig_cl.
InterPro; IPR003500; Ig_like.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; ig; 4.
SMART; SM00407; IG_like; 3.
SMART; SM00407; IGCl; 1.
PROSITE; PS00290; IG_MHC; 3.
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                                                   CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                          Hellman L., Pettersson U., Bennich H.; "Characterization and molecular cloning of the mRI (epsilon) chain of rat immunoglobulin E."; Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (IMMUNOCYTOMA STRAIN-LOU/C/WSL; MEDLINE=83064537; PubMed=6292865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 205-306 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A cloned cDNA probe for rat immunoglobulin epsilon construction, identification, and DNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kindsvogel W.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=83182019; PubMed=6820340;
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[1]
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Crea
21-JUL-1986 (Rel. 01, Last
15-JUL-1999 (Rel. 38, Last
Ig epsilon chain C region.
                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                modified
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                                                                                 Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1:335-343(1982).
                                                                                                                                                                                                                                              ,; J00744; AAA41379.1; ALT_INIT.
A02143; EHRT.
                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                  P01854;
                                                                                                                                                                                                                                                                                              requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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308
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                                   A,
                                                                                                  domain;
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nain; Immunoglobulin C
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chain from
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P01862;
                                                                                                                                                                                                            Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). 3. Amino acid sequence of thalf-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                              "Structure of heavy chain from strain 13 guin immunoglobulin-G(2). II. Amino acid sequence and hinge region cyanogen bromide fragments." Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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21-JUL-1986 (Rel. 01, Last
15-JUL-1999 (Rel. 38, Last
Ig gamma-2 chain C region.
                              SEQUENCE OF 134-226.
MEDLINE=75036072; PubMed=4429665;
                                                                                                                                               Turner K.J.,
                                                                                                                                                                MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                              SEQUENCE OF 4-68. MEDLINE=71058471;
                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1975)
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10141;
                 Tracey D.E., Cebra
                                                                                                                                                                               SEQUENCE OF 69-133 AND 312-329
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 Primary structure of
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01, Last sequence up
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Rodentia;
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l; Mismatches
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Hystricognathi; Caviidae;
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Best Local
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J.MOUSE STANDARD; PRT; 421 AA.
P06336; P01856;
21-JUL-1986 (Rel. 01, Created)

O1-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig epsilon chain C region.
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                                    NCBI_TaxID=10090;
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea
Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLAN
SEQUENCE
                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 13:4796-4803(1974).
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A02151; G2GP.
; P01842; 7FAB.
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IPR003600; Ig_like
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                                                      Chordata;
Rodentia;
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INTERCHAIN
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3; Mismatches
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                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                    Muridae; Murinae;
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InterPro; IPR003306; Iq_MHC.
InterPro; IPR003597; Iq_c1.
InterPro; IPR003600; Iq_like.
Pfam; PF00047; ig; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-84236092; PubMed=6329728; Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T. Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T. "The nucleotide sequence of the mouse immunoglobulin comparison with the human epsilon gene sequence."; EMBO J. 1:1117-1123(1982).
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requires a license agreement (See
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
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MEDLINE=89232738; PubMed=3149946;
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=85027161; PubMed=6092053;
Mels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00451; -; NO PIR; B02156; G3MSC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-AUG-1991
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Iransmembrane; Alternative splicing.
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FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                    QTPQVYTIPPPREQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGT
                                                        REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS
                                                                                                            VHTAWTQPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRA
                                                                                                                                                   VHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQP
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40, Last annotation update)
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Pred. No. 5.0
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CH2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003600; Ig_lik. Pfam; PF00047; ig; 3. SMART; SM00410; IG_like; 1. SMART; SM00407; IGCl; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J00451; AAB59655.1; EMBL; V01526; CAA24767.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wels J.A., Word C.J., Rimm D., Der-
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; |
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GC3M_MOUSE ST.
P03987;
23-OCT-1986 (Rel.
                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 328-398 FROM N.A. MEDLINE=84041483; PubMed=6314258;
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Komaromy M., Clayton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=85027161;
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-JUL-1999 (Rel. 3
gamma-3 chain C
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                                                                      12
                                                                                                                                          Similarity
                       PGSSCPPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKE 165
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                                               -CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
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; Ig_like.
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CH2.
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POTENTIAL.
CYTOPLASMIC (
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E -> Q (IN RI
E -> P -> F (IN RI
                                                                                                                                      Score 801.5; DB 1
Pred. No. 4.1e-48;
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EMBL; V00793; CAA24172.1; -. EMBL; V00793; CAA24173.1; -. EMBL; V00793; CAA24174.1; -.
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Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., S
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene
cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                        murine myeloma
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and complete nucleotide gamma 1 chain gene.";
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                                                                                                                                                                                                                                                                Svasti J., Milstein
                                                                                                                                                                                                                                                                                 MEDLINE=73008889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 76-324 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 18:559-568(1979).
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Takahashi N., Mano Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                             "Evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma-1 chain C
                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                         disulphide bridges of a mouse immunoglobulin G1 protein.";
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                                                                       s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                      gammal chain.";
253:6068-6075(1978).
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01, Last sequence up
39, Last annotation
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                                                                                                              is not removed.
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Sciurognathi; Muridae;
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CAA24175.

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AC P1C
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DT 115-
DT 15-
CC EUM
OC EUM
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Brueggemann M.;
Brueggemann M.;
"Evolution of the rat inv
Gene 74:473-482(1988).
Gene 74:473-482(1988).
PIR; PS0017; PS0017.
PO1842; 7FAB.
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PIR; A02159; G1
HSSP; P01842; 7
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SEQUENCE
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CONFLICT
                                                                                                                  GC1_RAT STANDARD; PRT; 326 AA. P20759; O1-FEB-1991 (Rel. 17, Created) O1-FEB-1991 (Rel. 17, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15 gamma-1 chain C region.
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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InterPro; IPR003006; Ig_MHC
InterPro; IPR003597; Ig_C1.
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HSSP; P01842; 7FAB.
G1ycoSuiteDB; P01868;
                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                    SEQUENCE FROM N.A. MEDLINE=89232738;
                                                                                NCBI_TaxID=10116;
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Sciurognathi;
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-> D (IN REF. 3)
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thi; Muridae; Murinae; Rat
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21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last seque
30-MAY-2000 (Rel. 39, Last annot
Ig gamma-1 chain C region, membr
Mus musculus (Mouse).
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC;
                                          SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197626; PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis
"MRNA for surface immunoglobulin gan
conserved transmembrane sequence and
                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                              "Cloning and complete nucleotide gamma 1 chain gene."; Cell 18:559-568(1979).
                                                                                                                          Honjo T., Obata M., Ya
Takahashi N., Mano Y.;
                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=80045036; PubMed=115593;
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InterPro; IPR003597;
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Rodentia;
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Mismatches
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and a
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a chains encodes
a 28-residue intr
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MEDLINE=82115295; PubMed=6799207

SEQUENCE OF 323-366

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U.S.A.

79:2008-2012(1982)

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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
PIR; B02159; GIMSM.
HSSP; P01842; 7FAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-82222190; PubMed-6283537;
Yamawaki Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED SPECIES APPEARS TO ENCODE MEMBRANT SPECIES APPEARS TO ENCODE MEMBRAND BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END. ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
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liternative splicing; Transmembrane.
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Search completed: July 15, 2003, 06:58:21 Job time: 18.7654 secs

GenCore version (c) 1993 - 2003

5:1.6 Compugen Ltd.

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ALIGNMENTS

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Hypothetical 51.8 kDa protein.
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Mammalia; Eutheria;
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PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                      ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                             EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                  NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                   ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51791 MW;
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97.0%;
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Pred. No. 1.6e-94;
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PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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RESULT 3
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ID Q8TC
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Best Local S
Matches 225
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PROSITE; PS00022; EGF_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01187; EGF_CA; UNKNOWN_1.

PROSITE; PS0011; GLU_CARBOXYLATION; UNKNOWN_1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                              INCEPTO: IPRO01881; EG1
InterPro: IPRO03006; Ig_
InterPro: IPRO01254; Ser_
InterPro: IPRO01254; VitK,
Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
MART; SM00181; EGF; 2.
OSTTE: PS00010.
Q8TC63;
Q8TC63;
01-JUN-2002
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Q96PQ8;
01-DEC-2001
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InterPro; IPR000561; EGF-like..
InterPro; IPR000742; EGF-2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR0013006; Ig_MHC..
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
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Homo sapiens (Human)
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225; Conserv
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Natl. Acad. Sci. (
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                                                                             NMYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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701 AA
 (TrEMBLrel.
                                                                                                                                                                                                                                                                          Conservative
                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or on tumor vascular endothelial cells and tumor yin mouse models of prostatic cancer."; U.S.A. 98:12180-12185(2001).
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                                                                                                                                                                                                                                                                         Score 1225; DB 4;
Pred. No. 2.8e-94;
3; Mismatches 4
                        PRT;
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Best Local :
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Q95M34;
Q1-DEC-2001
Q1-DEC-2001
                                                                                                     PROSITE;
                                                                                                                  InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_2:
                                                                                                                                                                                                                                     Wagner B., Overesch G., Sheoran A., Holmes Leibold W., Radbruch A.; "Organization of the equine immunoglobulin
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98383416; PubMed=9717671;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                     genes. III. Alignment
                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                genes. III. Alignment of c-mu, c
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
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TISSUE=KIDNEY;
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IGHC1.
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         al Similarity
157; Conserv
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473 AA; 5
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67.7%;
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                                                                                   MW;
         36;
       Score 877.5;
Pred. No. 1.6e
36; Mismatches
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Last annotation
chain constant a
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Pred. No. 9.
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                                                                                   A60BF2B01DEFD1F6
                                                                                                                                                                                                                   c-gamma,
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36;
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c-alpha genes.";
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Matches
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                                                                                                                                  Q99LC4 PRELIMINARY; PRT; 463 AA. Q99LC4; C1-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence up 01-JUN-2002 (TrEMBLrel. 21, Last annotation Similar to RIKEN cDNA 1810060009 gene.
                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (MAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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469 AA; 5
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Pred. No. 1.
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                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00400; IGcl; 2.
SMART; SM00400; IGcl; 2.
SMART; SM00410; IGcl; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                        Wilde K.G., Yu X., Ekramoddoullal "Cloning of cDNAs encoding for ar antibody (Mab 7, its light and he single chain antibody (ScFV)."; Submitted (MAY-1999) to the EMBL; AF152372; AAD40243.1; -. HSSP; PD1842; 7FAB.
                                                       Interety,

Pfam; PF0047; ig; 4.

SMART; SM00406; IGv; 1.

SMART; SM00410; IG_like; 2.

SMART; SM00290; IG_MHC; U
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Q9R1A4;
Q1-MAY-2000 (TIEMBLrel. 13, C
Q1-MAY-2000 (TIEMBLrel. 13, L
Q1-JUN-2002 (TIEMBLrel. 21, L
Gammal heavy chain of Mab7 (F
PROSITE;
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EMBL; BC003435; AAH034
HSSP; P01842; 7FAB.
MGD; MGI:96446; Igh-4.
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,P, P01842; 7FAB.

2; MGI:96446; Igh.4.

iterPro; IPR003600; Ig_like.

PPRO; IPR003006; Ig_MHC.

PRO; IPR00306; Ig_V.
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437 1
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463 AA; 51007 MW; EAA67
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                                                                                                                                                                                                                                                                                                                                                                                  Ekramoddoullah
  48142 MW;
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58.8%;
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Pred. No. 2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                 lah A.K.M., Misra S.; anti-white pine blister rust me heavy chains) and construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAA674C6BBC30783 CRC64;
  5C3A7BB3EE7D697C CRC64;
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HSSP; PO1842; /..

MGD; MGI:96443; Igh..

InterPro; IPR003599; Ig.

InterPro; IPR003597; Ig.cl.

"""O; IPR003600; Ig_like.

""O; IPR003006; Ig_MHC.

""AROUNG IG_MHC.
                                   SMART; SM00409;
SMART; SM00407;
SMART; SM00406;
SMART; SM00410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Sızuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Marchioni L., Mashima J., Mazzarolli J., Mombacarta D., Mashima J., Mazzarolli J., Manbacarta D., Mandali M., Mand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F. Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming I Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19, 18, 10060009RIK protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=PANCREAS;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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136; Conserv
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; IG; 2.
; IGc1; 3.
                                   IGv; 1.
IG_like; 1.
IG_MHC; UNKNOWN_1
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Rodentia;
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Pred. No. 4.1e-58;
7; Mismatches 41
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annotation update)
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InterPro; IPR003600; Ig_like.

InterPro; IPR003596; Ig_wHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 3.

R SMART; SM00409; IG; 2.

R SMART; SM00407; IGcl; 3.

R SMART; SM00406; IGv; 1.

R SMART; SM00410; IG_like; 1.

R PROSITE; PS00290; IG_MHC; UNKNOWN_1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2001)
EMBL; BC003878; AAHO:
HSSP; P01842; 7FAB
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                           FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                         YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
                                                                                                           REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.6%;
60.5%;
                                                                                                                                                                                                                                                                                                                                                     25.2%; Score 772; DB 1 62.9%; Pred. No. 2e-56; Live 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 782;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9DED57A514475FBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                Length 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Murinae; Mus
    468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT
Q99L25
ID Q99L25
ID Q9
AC Q9
DT 01

RESULT
1D 205
AC 0.00
DT 0.00
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Qy
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Best Local S
Matches 141
                                                                                                                                                                                                                                                                                                                                                           Q91Z05 PRELIMINARY;
Q91Z05;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Hypothetical 51.9 kDa pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2001) t
EMBL; BC003888; AAH038
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
51milar to RIKEN cDNA 1810060009 gene.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Rodentia; 'Sciurognathi; Muridae; Musimae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99L25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 1g; 3.

SMART; SM00409; IG; 2.

SMART; SM00407; IGC1; 3.

SMART; SM00406; IGV; 1.

SMART; SM00410; IGLike; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN 1.

PROSITE; PS00290; IG_MHC; UNKNOWN 1.

SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; InterPro;
                                  Strausberg R.; Submitted (JUL-2001) to the EMBL; BC010327; AAH10327.1;
                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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      MGI:2144967; AU044919
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41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IPR003599; Ig.
; IPR003597; Ig.cl.
; IPR003600; Ig.like.
; IPR003006; Ig_MHC.
; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPP--CPAPELLGGPSVFLFPPKDKLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPKGSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS
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                                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.2%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                  protein.
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19,
21,
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                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 772; DB
Pred. No. 2e-5
31; Mismatches
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                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                    Muridae;
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                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                    Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473
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                                                                                                                                                                                                                                    Mus
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RESULT 13
Q8VCX7
ID Q8VCX
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Q8R3H6
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PROSITE; PS00190; CYTOCHRO
PROSITE; PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                       OBR3H6;
O1-JUN-2002 (TrEMBLrel. 21, Cro
O1-JUN-2002 (TrEMBLrel. 21, Las
O1-JUN-2002 (TrEMBLrel. 21, Las
Hypothetical 51.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein SEQUENCE 473 AA; 5
                                                                                                                                                                                                                                                                      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; BC025447; AAH25447.1; -
Hypothetical protein.
SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874
                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8R3H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                Strausberg
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                    EDPEVKFNWYYDGVEVHNYKTKPREEQYNSTYRVYSVLTVLHQNWMNGKEYKCKVSNKAL
                                                                                                                                                                                             EPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                              ENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNYKTTPPYLDSVGSFFLYSKLTYDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPIEKTISKAKVQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPNIKDVLMISLTPKVTCVVVDVSE
                                                    NNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTE
                                                                                                                                                                                    EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE
                                                                                                                                                                                                                                                                                                                   R.
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOCHROME_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                      24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.6%;
58.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                                                                                                                                                                                                            Score 752.5;
Pred. No. 8.7e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 752.5; DB 1 Pred. No. 8.7e-55;
                                                                                                                                                                                                                                                                                                                                                         Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                     Craniata;
                                                                                                                                                                                                                                                                       8608B57C6CD2874A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                474
                                                                                                                                                                                                                                                                                                                                                                     Vertebrata;
                                                                                                                                                                                                                                        .7e-55;
                                                                                                                                                                                                                                                                                                                                                                                                   on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                 DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                             . 56;
                                                                                                                                                                                                                                                                                                                                                          Muridae;
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                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                          Murinae;
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Q8VCX7

PRELIMINARY;

PRT;

613

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RESULT
Q9BQB8
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AC Q9
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Best Local
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Interpro; IPR003597; Ig.cl.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003096; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00409; IGC1; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
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01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2002 (TrEMBLrel. 21, Last
01-JUN-2002 (TrEMBLrel. 21, Last
Hypothetical 67.9 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
Q9BQB8 PRELIMINARY; PKI; JJ, C...
Q9BQB8;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Unknown (protein for MGC:1905) (protein for MGC:1228).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2001) to the EMBL; BC018315; AAH18315.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 613 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=SALIVARY GLAND;
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                                                                                                                           TKGS-GF-FVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAV
                                                                                                                                                                               RAAPEVYAFATP--EWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRK
                                                                                                                                                                                                                           KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP
                                                                                                                                                                                                                                                                                           VSWLKDGKLVESGFTTDPVTIENKGSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLT
                                                                                                                                                                   HKHPPAVYLLPPAREQLNLRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMP
                                                                                                                                                                                                            EPLETKIKIMESHPNGTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISKPNEV
                                                                                                                                                                                                                                                    FLKNVSSTCAASPSTDILTFTIPPSFADIFLSKSANLTCLVSNLATYE-TLNISWASQSG
                                                                                                                                                                                                                                                                                                       IPAVAE--
                                                                                                                                                                                                                                                                                                                                                                           IQGIRTFPTLRTGGKYLATSQVLLSPKSILEGSDEYLVCKI-----HYGGKNRDLHVP
                                                                                                                                                                                                                                                                                                                                                                                           ----TPPVLDSVGSFFLYSKLTVDKSRWQQGN--VFSCSVMHEALHNHYQQRSLSLS--
                                                                                                                                                                                                                                                                                                                                                                                                                   TVTVSSESQSFPNVFPLVSCESPLSDKNLVAMGCLARDFLPSTISFTWNY----QNNTEV
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISKAKVQPREPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                                                                                                                                                                       -PGKVEGGGGSGGGSGGGSFTPPTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67855 MW; 41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.7%;
28.5%;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 480.5; DB 11; Pred. No. 9.5e-32;
                                                                                                                                                                                                                                                                                                                                    --MNPNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; |
thi; Muridae;
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Best I
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003066; Ig_w.
Pfam; PF00047; Ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 4.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNO; SEQUENCE 597 AA; 65300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2001) to the EMBL; BC006180; AAH06180.1; EMBL; BC001872; AAH01872.1; HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=MUSCLE;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LYMPH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mammalia; Eutheria;
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143; Conserv
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.1872; A...
.282; TFAB.; Ig.
.3; IPR003599; Ig.c1.
.703600; Ig_like.
.703600; Ig_MHC.
SILTVSEEEWNTGETYTCVVAHEAL-PNRVTERTVDKSTGK
                                                                                                                                                                                                                                      PVLDSVGSFFLYSKLTVDKSRWQQG---NVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPKDTLMISRTPEVTCVVVDVS-----HEDPEVKFNWYVD----GVEVHNVKTKPR
                                                                     PAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAH
                                                                                                       ATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVF
                                                                                                                                                               KQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SASAPTLFPLVSCENSPS----DTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFP
                                   SRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                            SHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLP
                                                                                                                                                                                                                    DQDTAIRVFAIPPSFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISE
                                                                                                                                                                                                                                                                                         SGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVP
                                                                                                                                                                                                                                                                                                                           VDLSTASTTQEGELA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCAD
                                                                                                                                                                                                                                                                                                                                                                                   SGGGGSGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.8%;
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Pred. No. 1.
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SMART; SM00409; IG; 2.

SMART; SM00407; IGC1; 4.

SMART; SM00406; IGV; 1.

SMART; SM00410; IG_11ke; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_3.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 65.3 kDa protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9BU10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00290;
Hypothetical prote
SEQUENCE 597 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR003599; Ig.
Interpro; IPR003597; Ig_cl.
Interpro; IPR003600; Ig_ilke.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC002963;
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480 PAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVLDSVGSFFLYSKLTVDKSRWQQG--NVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPKDTLMISRTPEVTCYVVDVS-----HEDPEVKFNWYVD----GVEVHNVKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPREPQVYTL-----PPSRDELTKNQVSLTCLVKGFYPSDIAVEWE-SNGQPENNYKTTP 180
                                               ATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVF
                                                                                                                                                                                                                                                                          SNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEE
                                                                                                                                                                                                                                                                                                                                        SGYTTDQVQAEAKESGPTTYKYTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGGGSGGGSFTPPTVKILQSSCDGGGHFPPTTQLLCLVSGYTPGTINITWLEDGQVMD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SASAPTLFPLVSCENSPS----DTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEQYNSTYRVVSVLTVLHQNWMNGKEYKC-KVSNKALPAPIEK-----TISKAKV 126
                                                                                                          SHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLP
                                                                                                                                             KQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-
                                                                                                                                                                                                                          DQDTAIRVFAIPPSFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISE
                                                                                                                                                                                                                                                                                                                                                                                             VDLSTASTTQEGELA-----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVLRG-GKYAATSQVLLPSKDVMQGTDEHVVCKVQHP---NGNKEKNVPL-PVIAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVG
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597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.7%; Score 448.5; DB 4; Length 24.6%; Pred. No. 4.5e-29; tive 96; Mismatches 267; Indels
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Search completed: July 15, 2003, 07:01:49 Job time: 64.9554 secs

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                                                                                                                                                                                                                                                                              Score
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2: /SIDS2/gcgdata/gc
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1 EPKSCDKTHTCPPCPAPELL.....HEAASPSQTVQRAVSVNPGK 569
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Human Ig-E heavy c
Sequence of human
Human IgE heavy ch
Human IgE heavy ch
Human IgE heavy ch
Human IgE C2-C3-C4
Human IgE C2-C3-C4
Fc(epsilon) CH2'-C
                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                 Human IgE heavy ch
Human IgE epsilon
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	AAY72915)))	222	40.0	1225
	AAB28690	21	232	0.	N
	AAW26232	18	232	40.0	22
vy chair	AAW48650	19	652	0	22
EPO	ABB73415	23	253	0	22
Fc-EMP protein	AAB16964	21	253		N
Recombinant	AAW49073	19	379	0	22
bin.	AAW83962	19	379	0	22
co	AAB31694	22	660	0	23
	AAB70132	22	660	0	23
Ectromelia A3	AAB28523	21	660		23
-	AAY13463	20	660		23
Fc-huAGP-1 (114	AAB28693	21	423		32.
Humanised HMFG-	AAM52159	22	741	•	•
Humanised HMFG-1	AAM52156	22	731	•	234.
\rightarrow	AAB28695	21	426	•	4
GP-1	AAB28694	21	448	•	Ν
	AAY96531	21	269	•	4
TMP-TMP	ABB73412	23	268		4
Fc-TMP-TMP protein	AAB16959	21	268		4
EMP-EMP	ABB73418	23	277	•	1247
MP-EMP p	AAB16967	21	277	•	1247
1-FD-	AAY96779	21	689	•	1251.5
GH-	AAY96780	21	689		h 1
I fusi	AAW85692	20	711		6.3
man IgE C2	AAU80289	23	330	54.6	1671
epsilon)	AAR85582	16	315	•	~
o CH4	AAR83582	16	325	55.1	1685
Human IgE heavy	AAU80288	23	336	55.4	1696
n immunc	9	21	325	•	1701
leukin-2	2	9	367	•	1707
n IğE	0364	21	331		1707
IGE F	R772	16	325	55.8	
Human IgE Fc	AAR75225	16	325	•	1707

ALIGNMENTS

AAU80283 standard; Protein; 428 AA

Human IgE heavy chain C1-C2-C3-C4 domains

30-JUL-2002 (first entry)

AAU80283;

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IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
Regior
                 Region
                                                                                      Region
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                                                   /note= "I
217..316
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209..216
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113. 208
/note= "Epitope in BC
244..251
/note= "Epitope in BC
272..280
                /note= "Epitope in BC loop"
                                                                                      /label= IgE heavy chain C2
205..219
                                                                                                                        Location/Qualifiers 11..116
                                           /note=
                                        "IgE heavy chain C3 domain"
                                                            "Linker
                                                                             "Epitope including C2C3 linker"
                                                                                                               "IgE heavy chain C1 domain"
                                                            domain between C2 and C3
         loop'
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Best Local S
Matches 347
                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in an animal, which is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic the human IgE heavy chain C1-C2-C3-C4 domains used to create the epitopes of the invention.
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Examples; Page 101-103; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inducing
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15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g immune response against autologous immunoglobulin E in an
by effecting simultaneous presentation of cytotoxic T
yte epitope an/or B-cell epitope derived from the immunoglobulin
                                                                                                                                                                                                                                                                                      Similarity
              PSPFDLFTRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                  GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 304
                                                                                                                                                                                                                 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL
PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                        --SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                                                                                                                                                              SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC-------
                                                                                                                                                                                       VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGGGGGG
                                                                                                                                                                                                                                            REPOVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
                                                                                                                                                                                                                                                                      57.7%;
nilarity 78.0%;
Conservative 1
                                                                                                                                                                                                                                                                                                                               428 AA;
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2000US-232831P
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315..323
/note= "E
317..320
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321..4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "IgE heavy chain C4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Epitope including C3C4 linker"
                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Voldborg
                                                                                                                                                                                                                                                                      Score 1766; DB 23;
Pred. No. 9.5e-115;
7; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
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        The present sequence is that of the human IgE epsilon chain constant region. The invention is based on the discovery that a polypeptide that includes the CHI (i.e. constant domain I in the heavy chain) and/or CH4 domain(s) of an IgE molecule, coupled to a carrier, can be used to induce in a mammal the production of antibodies that specifically bind to IgE of the mammal. Compositions are provided for inducing self-specific anti-IgE antibodies. These contain carriers foreign to the immunised mammal coupled to polypeptides containing fragments of the IgE molecule, especially fragments including the constant CH1 and/or CH4 domain, but not the CH3 domain. CH1 polypeptides have at least 95% identity to amino acids 1-110, 105, 5-105 or 5-95 of the present sequence, while CH4 nolypoptides have at least 95% identity.
                                                                                                                                                                                                                       Composition for treating immunoglobulin (Ig) E-mediated disorder such as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises a polypeptide that includes CHI and/or CH4 domains of IgE molecule coupled to a carrier
while CH4 polypeptides
                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                (CYTO-)
(BACH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGE; immunoglobulin E; antibody; human; allergy; asthma; eczema; urticaria; anaphylactic shock; allergic rhinitis; conjunctivitis; antianaphylactic; immunosuppressive; antiallergic; antiasthmatic; antianaphylactic; immunosuppressive; antiallergic; antiasthmatic; antiinflammatory; dermatological; vasotropic; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM50940;
                                                                                                                                                                                               Claim 41; Page 9; 71pp; English.
                                                                                                                                                                                                                                                                                                                        Bachmann MF,
                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000;
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Best Local S
Matches 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                administered. The compositions and polynucleotides are used to inhibit or treat IgE-mediated disorders such as anaphylactic shock, allergic rhinitis or conjunctivitis, an allergic reaction an allergen such as fur, dust or food, an asthmatic reaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eczema or urticaria (all claimed).
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                     28-APR-2000; 2000US-200298P
                                                            28-APR-2001; 2001WO-US13932
                                                                                                      08-NOV-2001
                                                                                                                                           WO200183529-A2
                                                                                                                                                                                                                             transgenic
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human rhinovirus; immu
                                                                                                                                                                                                                                                                                                            Human Ig-E heavy
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unoglobulin heavy chain;
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Pred. No. 9.5e
17; Mismatches
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9.5e-115;
nes 57;
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                                                                                                                                                                                                                                                ICAM-1;
HRV; co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                  common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                cold;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364
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                                                                               Db
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Best Local
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                                                                                                                      485
                                                                                                                                                                284
                                                                                                                                                                                                                                                224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGGS
                                          ICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                      ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                      LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                                                                PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                     PSPEDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                               STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                                                                                                       STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                                                                                                                                                            GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA--SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPQYYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
                                                                                 ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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57.7%; 78.0%;

Score 1766; Pred. No. 9. Mismatches

DB 23;).5e-115; hes 57;

Indels Length

24;

Gaps

185

62

163 304 105 244

484

283

403

424 223 364 17;

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reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty capsids. Expression of the immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than in animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an immunoadhesin comprising:
(a) a chimeric intercellular adhesion molecule (ICAM)-1 comprisin rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
                                                                             since plants are not known sequence is that of a human the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and secretory component in association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoadhesin for treating human rhinovirus chimeric intercellular adhesion molecule-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PLAN-) PLANET BIOTECHNOLOGY
428
    AA;
                                                                                                                                a human
                                                                                                                           immunoglobulin protein sequence, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and optionally a J chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising
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RESULT 4
AAP40065
ID AAP4
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                           DNA encoding IgE H-chain and frags. is claimed (AAN40062). Transformant contg. the DNA is also new, esp. Escherichia coli IFO-14284, -5 and -6. The transformant may be grown to produce a polypeptide of immunological or biological activity equivalent to that of the human IgE H chain. AAN40062 or frags. is pref. linked a site downstream from a promoter, e.g. rec A promoter (see AAN40064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide having activity of human immunoglobulin from host transformed with recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP102634-A.
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kikuchi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP40065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP40065 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1984-070437/12.
    341
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                                                   281
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                                                                                                  221
                                                                                                                       297
                                                                                                                                               168
                                                                                                                                                                      237
                                                                                                                                                                                              119
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                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                            349;
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAN40062
GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWP
             GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWP
                                               GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN
                                                             GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN
                                                                                                            MDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPR
                                                                                                                                                          GGSGGGGSGTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQV
                                                                                                                                                                                                              TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGG
                                                                                                                                                                                            TLPATTLTLSGHYATISLLTV-SGAWAK-QIFTCRVAHTPSSTDWVDNXTF---
                                                                                                                                                                                                                                          TVSSASTQ--SPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTM 118
                                                                                                                                                                                                                                                                 TISKAKVQPREPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of human
                                                                                               MDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPR
                                                                                                                                              ----SVCSRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQV
                                                                                                                                                                                                                                                                                                                                        493 AA;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kurokawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83EP-0108699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin E H-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                   57.5%;
77.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IND KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onda
                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493
                                                                                                                                                                                                                                                                                        Score 1760; DB 5;
Pred. No. 3e-114;
4; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₿
                                                                                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                                                Length 493;
                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                        Gaps
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                                                                       416
                                                                                                                      356
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                                                340
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RESULT 5
AAU80287
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Inducing immune response against autologous immunoglobulin E in animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunog
                               WPI;
                                                                           06-SEP-2000;
15-SEP-2000;
                                                                                                 06-SEP-2001; 2001WO-DK00579
                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                  heavy
                                              Klysner
                                                             (PHAR-) PHARMEXA AS
                                                                                                                 14-MAR-2002.
                                                                                                                                WO200220038-A2
                                                                                                                                                       Domain
                                                                                                                                                                                   Region
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                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 IgE; allergy;
antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU80287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU80287
                                                                                                                                                                                                                                                                                                                                                                                                                        Human IgE heavy chain C1-C2-C3-C4 domains with MIGIS fragment
                               2002-383033/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477
                                                                                                                                                                                                                                                                                                                                                                                  chain
                                              s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EWEQKDEFICPAVHEAASPSQTVQRAVSVNPGK
                                             Von Hoegen
                                                                           2000DK-0001326
2000US-232831P
                                                                                                                                                                                                                                                                                                                                                                                 dermatological; antiinflammatory; immunoghylaxis; allergic rhinitis; asthma; atopic domain; MIGIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                         human;
                                                                                                                                                                                                                                                                            /note= ")
217..317
                                                                                                                                                    321..422
/note= "IgE heavy chain
                                                                                                                                                                                   /note=
318..3
                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                        /note=
113..2
                                                                                                                                                                                                                                 272..280
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 11..106
                                                                                                                                                                                                  315..323
                                                                                                                                                                                                                  301..311
                                                                                                                                                                                                                                               244..251
                                                                                                                                                                                                                                                                                           209..216
                                                                                                                                                                           /note=
                                                                                                                                                                                                                          /note-
                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                    /note-
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                                                                                                                                                                                                                                                      'note
                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                   ..320
                                                                                                                                                                                                                                                                                                                        ..208
                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                        antiallergic;
                                              P,
                                                                                                                                               "MIGIS fragment"
                                                                                                                                                                           "Linker
                                                                                                                                                                                          "Epitope including C3C4
                                                                                                                                                                                                          "Epitope
                                                                                                                                                                                                                        "Epitope
                                                                                                                                                                                                                                      "Epitope
                                                                                                                                                                                                                                                                   "IgE heavy chain C3
                                                                                                                                                                                                                                                                                                 "Epitope including C2C3 linker"
                                                                                                                                                                                                                                                                                                                              "IgE heavy
                                                                                                                                                                                                                                                     "Epitope in
                                                                                                                                                                                                                                                                                  "Linker
                                                                                                                                                                                                                                                                                                               IgE heavy chain
                                             Voldborg
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                                                                                                                                                                           between domains
                                                                                                                                                                                                                                                                                  domain
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                                                                                                                                                                                                          FG
                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                         DE loop"
                                                                                                                                                                                                                                        ВС
                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressive; antianaphylactic;
linflammatory; immunoglobulin E; IgE;
                                              В,
                                                                                                                                                                                                          loop"
                                                                                                                                                                                                                                       loop"
                                                                                                                                                                                                                                                     loop"
                                                                                                                                                                                                                                                                                   between C2 and
                                                                                                                                                            C4
                                                                                                                                                                                                                                                                                                                C2
                                                                                                                                                                                                                                                                                                                               CI
                                              Gautam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493
                                                                                                                                                            domain"
                                                                                                                                                                                                                                                                    domain"
                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                               domain"
                                                                                                                                                                            C
                                                                                                                                                                                           linker"
                                                                                                                                                                            andC4"
                                                                                                                                                                                                                                                                                    င္ပ
                                                                                                                                                                                                                                                                                  region"
                                                                                                                                                                                                                                                                                                                                                                                         dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460
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immunoglobulin

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ARRESULT 6
ARAR429C
IID AAR4
XX
AC AAR4
XX
DT 12-P
XX
XX
KW Inmmu
KW FCR
KW tarc
XX
OS Homc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel method for inducing an immune response cagainst autologous immunoglobulin E [Ig] in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTI) epitope and/or B-cell epitope derived from IgE, and T helper cell cepitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) or the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating cutologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic crininitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C1-C3-C4 domains fused to the MIGIS CC fragment used to create the epitopes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                 AAR42950 standard;
                                    Immunoglobulin E; IgE;
FCR region; allergen; a
                                                                                                 12-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 REPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
                                                                                                                                                                                                              404
                                                                        IgE heavy chain constant region (residues 120-547).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL
                                                                                                                                                                                                                         ICRAVHEAASPSQTVQRAVSVNP 567
                                                                                                                                                                                                                                                            ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                    ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                                                        LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                                                                                                                                                                            PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                                                                        PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                                                                                                            STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGHYATISLLTV-SGAWAK-OMFTCRVAHTPSSTDWVDNKTFSVC---
                                                                                                                                                                                                              ICRAVHEAASPSQTVQRAVSVNP
                                                                                                                                                                                                                                                                                                            LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
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                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                protein;
                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.48;
77.98;
                                    ; epsilon heavy chain; IgE receptor binding;
allergic reaction; catalytic antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151pp; English.
                                                                                                                                                 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1755;
Pred. No. 5
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5.7e-114;
nes 57;
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Query Match
Best Local
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catalytic antibodies which cleave specific target sequences in the IgE heavy chain constant region are exemplified. Cleavage is targetted so as to separate the Fab (antigen binding region) from the Fc region (contg. FcR binding site for attachment to the IgE receptor on mast cells), thereby destroying receptor binding activity. The target peptides were selected after consideration of their primary and secondary structure. The antibodies can be used to block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selecting catalytic antibodies which cleave target peptide - to block allergic reactions or as preventive treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davis CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-SEP-1990;
22-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 3; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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                                     486
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                                                                                                                                                                                                                                                                                             105
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                                                                                                                                                                                                                                                                                                                               246
                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 REPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
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VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSGGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                     QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL
                                                                       PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATREWPGSRDKRTLA
                                                                                          PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLA
                                                                                                                                               SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                     TTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSATLSRP
                                                                                                                                                                                                                                        TTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRP
                                                                                                                                                                                                                                                                                                                                                                 SGHYATISLLTV-SGAWAK-QMFTCRVAH-----TPSSTDWVDNKTE-----SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 AA;
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91US-0780765
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193..22
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181..257
/label= FcR_binding_region
/note= "residues 301-376 of IgE H chain,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in binding to IgE receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1723; DB 14; Pred. No. 9.3e-112;
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                   This invention relates to a novel method for inducing an immune resagainst autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphc (CTL) epitope and/or B-cell epitope derived from IgE, and T helper epitope (TH epitope) which is foreign to the animal, by antigen
                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2000;
15-SEP-2000;
                                                                                                                                                Disclosure;
                                                                                                                                                                                                     Inducing immune response against autologous immunoglobulin E in animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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heavy chain C domain.
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                                                                                                                                              Page 105-106;
                                                                                                                                                                                                                                                                                                                                 Von
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2000US-232831P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         numan; antiallergic; immunosuppressive; antianaphylactic;
dermatological; antiinflammatory; immunoglobulin E; IgE;
ylaxis; allergic rhinitis; asthma; atopic dermatitis;
                                                                                                                                                                                                                                                                                                                                   Hoegen
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210..2
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139..145
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104..111
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216..3
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167..1
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112..2
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196..2
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                                                                                                                                                                                                                                                                                                                                 P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Epitope including C3C4 linker"
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                                                                                                                                              151pp; English
                                                                                                                                                                                                                                                                                                                              Voldborg
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WPI; 2002-383033/41 N-PSDB; ABK51133.

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                                                                                      06-SEP-2000;
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Synthetic.
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antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
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Pred. No. 8.4e-111;
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antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; Iç
vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
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by effecting simultaneous presentation of cytotoxic T
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by effecting simultaneous presentation of cytotoxic
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                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                          Score 1707; DB 23;
Pred. No. 8.4e-111;
0; Mismatches 0;
323
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RESULT 10 AAR83559 ID AAR83

AAR83559

standard;

Protein;

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NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 549

490

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cc 266BL cDNA library screened with a probe corresp. to the N-terminus of CC 19E. The region encoding amino acids 218-547 was cloned into the vector cc pwT311 under control of the tryptophan promoter. The resultant protein CC replacing their coding sequence with a bicistronic linker. The resultant CC construct encodes the Fc(epsilon) constant heavy region from amino acids CC 226-547. When it is expressed in E.coli, the protein produced is a CC qlycosylation unmasks new antigenic sites thus rendering the Fc fragment immunogenic and able to induce antibodies that recognise native IgE but CC in anti-allergenic vaccines to modulate the fragments complexes. The Fc fragments can he nearly constant the constitution constant heavy region from anion acids cc 10 do not form histamine-releasing complexes. The Fc fragments can he nearly constitution in anti-allergenic vaccines to modulate that recognise native IgE but C mediated he recognise can be nearly complexes.
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                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 320
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has epitope(s) not present in native IgE, also derived antibodies for treating or preventing allergies, inflammatory immune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;
constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
histamine; anti-allergenic; vaccine; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 32-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR83559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-1994;
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diated by IgE.
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                                                         LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                        FIPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                 RDWIEGETYQCRVTHPHLPRALMRSTIKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                         GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 369
                                                                                                                                                                                                                      FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                 324 AA;
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                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94FR-0000846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  French
                                                                                                                                                                                                                                                                  Score 1707; DB 16; Pred. No. 8.5e-111;
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RESULT 11
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                           The sequence represents a chain (amino acids 224-54)
                                                                Mutated glycosylated polypeptide(s) useful to study and treat allergy.
                                                                                                             Gould
                                                  Disclosure; Page 6;
                                                                                              WPI; 1995-206936/27
                                                                                                                           (THRE-) 3I RES EXPL LTD. (CLLT ) CELLTECH THERAPEUTICS
                                                                                                                                                 22-NOV-1993;
                                                                                                                                                                22-NOV-1994;
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          represents a mutant sequence of a human IgE-F (amino acids 224-547) which is of sufficient length silon RI and/or Fc-epsilon FII IgE receptor sites on . The protein is useful in the study and .....
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                                                                                                             Owens
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172
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Gaps

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human IgE Fc chain (amino acids
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       Disclosure;
                                                 Mutated glycosylated polypeptide(s) contg. useful to study and treat allergy.
                                                                                                                     WPI; 1995-206936/27
N-PSDB; AAQ91170.
                                                                                                                                                                                                                                                                                                                                                            22-NOV-1994;
                                                                                                                                                                                                                                      (THRE-) 3I RES EXPL LTD. (CLLT ) CELLTECH THERAPEUTICS
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                                                                                                                                                                                          Owens RJ,
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  Page 35-36;
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172
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55pp; English.
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RESULT 13
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XX AAB03
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Best Local S
Matches 320
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                                                                                                                                                                                                                                                                                                                                                       11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                             WPI; 2000-365342/31
                                                                                                                                                                                                                                        02-NOV-1998;
22-SEP-1999;
                                                                                                                                                                                                                                                                                                             21-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human IgE heavy chain constant regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB03642 standard;
                                                                                                                                                                                       (RESI-) RESISTENTIA PHARM AB
                        Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEAASPSQTVQRAVSVNPGK 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
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99US-0401636.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgE; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 14
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Best Local S
Matches 320
                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2, 3 and 4 of the human IgE. It was used to construct a number of immunogenic peptides which consisted of regions of IgE from different mammals, which appear to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
                                                                                                                                                                        EP269455-A.
        18-GEP-1987;
                                                             27-NOV-1987;
                                                                                                                    01-JUN-1988
                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-2/IgE Fc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEAASPSQTVQRAVSVNPGK 331
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llarity 100.0%;
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                                                                                                                                                                                                                                /label
                                                                                                                                                                                                                                                                                                                                                                         /label=IL-2 leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 /label=IL-2 N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fc receptor; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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Pred. No. 8.7e-111;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; asthma; dermatitis
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AAY79994
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AC AAY7
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Immu
KW Immu
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PR 20-0
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     20-JUN-1998;
                                                          21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430
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Query Match
Best Local Similarity
Matches 320; Conserv
                                                                                                                                            Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell er antibody; allergy; allergic disease; immunisation; anti-allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-terminal
                              29-DEC-1999
                                                               WO9967293-A1
                                                                                                                             anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis;
                                                                                                                                                                                                               Human immunoglobulin E epsilon heavy chain SEQ ID
                                                                                                                                                                                                                                                  15-MAY-2000
                                                                                                                                                                                                                                                                                                                 AAY79994 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fused protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1988-149211/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s fusion protein has a low toxicity and is useful in therapy allergy induced by IgE. It can be used in the treatment of ergic dermatosis, atopic dermatitis or bronchial asthma.
                                                                                                sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                              550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ein for allergy treatment - comprising interleukin-2
residues, a linker and human immunoglobulin E Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.8%; Score 1707; DB 9; llarity 100.0%; Pred. No. 9.9e-111; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                (first
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99WO-US13959
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                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                               dermatitis
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                                                                                                                                                               epitope;
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98US-0100287

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                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes immunoglobulin E (IgE)-CH3 domain CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic CC and anti-asthmatic properties. (I) induces polyclonal antibodies Specific for a target effector site on the ppsilon-heavy chain of IgE, CC and so preventing triggering and activation of mast cells and basophils CC and downregulation of IgE synthesis. Conjugates, or fusion peptides, CC containing (I) are used for active immunisation against IgE-mediated CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy CC dermatitis. Nucleic acids that encode these compounds are useful for CC recombinant production of corresponding peptides or in DNA vaccines. CC Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell CC constraints (disulfide bridge) to stabilise conformational features and CC maximize cross-reactivity to the natural target. They induce safe CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.6%;
Best Local Similarity 99.4%;
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 66-68; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antigenic peptide from the CH3 domain of immunoglobulin {\tt E}, fusions for immunization against allergy -
490
                                                                                                                                                                                                                      126
                                                                                                                                                                                                                                                          370
                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                186
                                                                                                                                                                                    430
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                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                           GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                       LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 429
                                                                                           NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 549
                                                                                                                                                                 RDWIEGETYQCRVTHPHLPRALMRSTIKTSGPRAAPEVYAFAIPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                    LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                        NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWQEKDEFICRAV 305
                                                                                                                                              RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1701; DB 21;
Pred. No. 2.2e-110;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                              245
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                                                                                                                                                                                  489
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Search completed: July 15, 2003, 06:57:41 Job time: 68.0009 secs

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Result
No.
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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Maximum Match 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on:
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1707
1705.5
1696
1671
                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA:*

1: //gqn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

2: //gqn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: //gqn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: //gqn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

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6: //gqn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: //gqn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

9: //gqn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

10: //gqn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

11: //gqn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

12: //gqn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

13: //gqn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

14: //gqn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

14: //gqn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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length: 2000000000
  BLOSUM62
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3060
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                                                                                                                                                                                                                                                                                 Query
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                   Length
  DB
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  US-09-847-208-7
US-10-214-524-35
US-10-214-524-35
US-09-847-208-5
US-09-949-375A-7
US-09-949-375A-3
US-09-949-375A-6
US-09-949-375A-1
US-10-216-53-329
0 US-09-949-375A-1
0 US-09-949-375A-1
                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (without alignments)
1517.518 Million cell updates/sec
                                                                                                                             Sequence 7, Appli
Sequence 45, Appli
Sequence 37, Appli
Sequence 5, Appli
Sequence 60, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 34, Appli
Sequence 34, Appli
            Sequence 7
Sequence 6
Sequence 2
Sequence 4
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Sequence 1
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Sequence 2
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                          6 Appli
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45	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1227	1232	1234.5	1234.5	1260	1260	1273.5	1364.5	1435.5	1566.5	1579	1649
40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.1	40.3	40.3	40.3	41.2	41.2	41.6	44.6	46.9	51.2	51.6	53.9
332	331	330	330	330	330	288	288	267	251	251	247	235	232	543	660	741	731	330	232	711	346	346	348	347	347
9	9	9	9	9	9	9	9	10	9	9	10	9	10	9	9	10	10	9	9	9	φ	ဖ	9	9	9
US-09-990-586-98	US-10-341-836-2	US-10-269-805-68	US-09-892-949-38	US-09-995-898A-15	US-10-047-542-20	US-10-119-637A-14	US-09-822-851B-14	US-09-996-357-12	US-10-152-363A-6	US-10-008-063-18	US-09-996-357-13	US-10-207-655-208	US-09-996-357-10	US-10-207-655-345	US-10-294-055-8	US-09-825-012-55	US-09-825-012-46	US-09-847-208-2	US-09-847-208-3	US-10-071-485-90	US-10-152-190-14	US-10-152-190-10	US-10-152-190-11	US-10-152-190-12	US-10-152-190-13
98,	Sequence 2, Appli	68,	Sequence 38, Appl	Sequence 15, Appl	•	Sequence 14, Appl	Sequence 14, Appl	Sequence 12, Appl	Sequence 6, Appli	Sequence 18, Appl	Sequence 13, Appl	8,		Sequence 345, App	Sequence 8, Appli	Sequence 55, Appl	Sequence 46, Appl	Sequence 2, Appli	Sequence 3, Appli	`	•	Sequence 10, Appl		Sequence 12, Appl	Sequence 13, Appl

ALIGNMENTS

```
APPLICANT: SAXON, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
FITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
FITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 569
TYPE: PRT
ORGANISM: Unknown
                                                                                                                                            DЪ
                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4; OTHER INFORMATION: (IgE)
US-09-847-208-7
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US-09-847-208-7
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                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                  121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                               569;
                     181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSG
                                                                                                                                            61 NWYYDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                  61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                               1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                    1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                            ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
Conservative
                                                                                                                                                                                                                                                                                                                                100.0%; Score 3060; DB 9; 100.0%; Pred. No. 8.5e-181;
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Sequence 45, Application US/10047542

Patent No. US20020168367A1

GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRA

TITLE OF INVENTION: AND BACTERIAL DISEASES

FILE REFERENCE: 030905.0004.CIP1

CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR APPLICATION NUMBER: DOS-04-28

PRIOR APPLICATION NUMBER: DOS-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR ELING DATE: 2000-04-28

PRIOR ELING DATE: 2000-04-28

PRIOR ELING DATE: 2000-04-28

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; ORGANISM: HOMO
US-10-047-542-45
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US-10-047-542-45
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 RGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR
                                                                         VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP
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                                                                                                                                                                                                 TLPATTLTLSGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC-----
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77.3%;
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PRIOR FILING DATE: 2001-08-13
NUMBER OF SEO ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEO ID NO 37
LENGTH: 574
TYPE: PRT
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; Publication No. US20
; GENERAL INFORMATION:
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Best Local Similarity
Matches 351; Conserv
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FILE REFERENCE: IGE-00101.P.1.1

CURRENT APPLICATION NUMBER: US/10/214,524

CURRENT FILING DATE: 2002-08-08

CURRENT FILING DATE: 60/312,120
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APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES
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AEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                 NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW
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No. US20030073142A1
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77.3%;
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Pred. No. 1.1e-101;
L7; Mismatches 60;
574
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355

235 251

360

Length 428; Indels

24;

Gaps

62

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US-10-047-542-60

Sequence 60, Application US/10047542

Patent No. US2020168367A1

GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.

APPLICANT: MYCOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING ANT TITLE OF INVENTION: AND BACTERIAL DISEASES

FILE REFERENCE: 030905.0004.CIP1

CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-10-26

CURRENT FILING DATE: 2001-10-26
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APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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; TYPE: PRT
; ORGANISM: Homo s
US-09-847-208-5
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Best Local Similarity
Matches 347; Conserv
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Pred. No. 2.8e-101;
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; LENGTH: 428
; TYPE: PRT
                                                                                                                                                                                           APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09949375A Patent No. US20020172673A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
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            NAME/KEY: MISC_FEATURE LOCATION: (209)...(216) OTHER INFORMATION: Linker
                                                                                             FEATURE:
NAME/KEY: DOMAIN
LOCATION: (11)..(116)
                                                                                                                                                              LENGTH: 428
TYPE: PRT
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                                                                               OTHER INFORMATION: Human
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; LOCATION: (113)..(208)
; OTHER INFORMATION: Human IgE heavy chain
US-09-949-375A-1
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OTHER INFORMATION: Epitope
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LOCATION: (217)..(316)
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                                            ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF 544
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Pred. No. 2.8e-101;
7; Mismatches 57;
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US-09-949-375A-7

Sequence 7, Application US/09949375A Patent No. US20020172673A1 GENERAL INFORMATION:

APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7

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US-09-916-230-1
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SEQ ID NO 1
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Patent No. US20020146422A1
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TYPE: PRT
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404 ICRAVHEAASPSQTVQRAVSVNPGK 428
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all Similarity 78.0%;
347; Conservation
                                                                                                                                                                                           224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 REPOVYTLPPSRDELTKNOVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                             186 VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGG
                                                        ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                           LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                          LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                          PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                 GGGGSTTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA--SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA-
                  ICRAVHEAASPSQTVQRAVSVNPGK 569
                                                                                                                                                                                                                                                       STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                        STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL
                                                                                                                                                                                       PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1766; DB 10;
Pred. No. 2.8e-101;
.7; Mismatches 57;
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Jses Thereof
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Best Local S
Matches 345
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LOCATION: (301)..(311)
OTHER INFORMATION: Epitope in
-09-949-375A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: DOMAIN
LOCATION: (427)..(441)
OTHER INFORMATION: MIG
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE LOCATION: (272)..(280) OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC_FEATURE LOCATION: (244)..(251) OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (315)..(323)
OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE LOCATION: (205)..(219)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (318)..(320)
OTHER INFORMATION: Linker
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OTHER INFORMATION: Linker
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LOCATION: (321)...(4
OTHER INFORMATION:
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NAME/KEY: DOMAIN
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OTHER INFORMATION:
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                                                                                                                                                                                                                              REPOVYTLPPSRDELTKNOVSLT - - CLVKGFYPSDIAVEWESNGOPENNYKTTP - PVLDS
                                                                         GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 304
--SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 163
                                                                                                                                      SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC------
                                                                                                                                                                                                  QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL
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                STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                              STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR 364
                                                                                                                                                                                                                                                                Conservative
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ION: IGE
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DN: IGE
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77.9%;
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Pred. No. 1.4e-100;
7; Mismatches 57;
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SEQ ID NO 334
LENGTH: 592
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-10-207-655-334
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No. US20030118592A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST 424
                KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP
                                                                                                                TPGTINITWLEDGQVMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGH
                                                                                                                                      TPGTINITWLEDGQVMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGH
                                                                                                                                                                                   YYSNSYWYFDVWGTGTTVTVSDHVCSRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGY
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KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP
                                                         TFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG
                                                                                                                                                                                                                                                                                                        LELKGGGGGGGGGGGGSQAYLQQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQT
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                                                                         TFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG
                                                                                                                                                                                                                                             PRQGLEWIGATYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVV
                                                                                                                                                                                                                                                                                                                                                                     SGVPARFSGSGSGTSYS-LTISRVEAEDAATYYC-----QQWSFNPPTFGAGTK 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.5%; ilarity 60.9%; Conservative
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Pred. No. 7.7e-99;
5; Mismatches 51
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Gaps

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304 281 244 249

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В δÃ 밁 οy

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Sequence 2, Application US/09949375A
Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IG:
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SAXON, ANDREW
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
ITITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION UNMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 320
                                                                                                                                                                          US-09-949-375A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-847-208-6
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Matches 320;
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NAME/KEY: MISC_FEATURE
LOCATION: (100)..(114)
OTHER INFORMATION: Epito
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LOCATION: (196)..(206)
OTHER INFORMATION: Epitope
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LOCATION: (210)..(218)
OTHER INFORMATION: Epitope
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LOCATION: (216)..(317)
OTHER INFORMATION: Hum
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                                                          ; OTHER INFORMATION: US-09-949-375A-6
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APPLICANT: KLYSNER, Steen et al.
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                         Sequence 6, Application US/09949375A
Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
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                                                                                                                               CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
DENOTH: 323
                             Query Match
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Best Local
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ORGANISM: Artificial Sequence
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US-10-176-664-1
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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Best Local Similarity
Matches 320; Conserv
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PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
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                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 331
TYPE: PRT
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Pred. No. 9.1e-98;
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CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 329
LENGTH: 331
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-10-207-655-329
Search completed: July 15, 2003, 07:17:20 Job time: 44.6521 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069,401C1
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Pred. No. 9.1e-98;
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                                                                                             TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: --to be ass
APPLICATION NUMBER: conversion
FILING DATE: October 26, 1998
CLASSIFICATION:
TOPOLOGY: 11 MOLECULE TYPE:
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (206)470-4189
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Melanie K. Spriggs, Michael R. Comeau, APPLICANT: Robert F. DuBose, Richard S. Johnson TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTTITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: U
APPLICATION NUMBER: P
FILING DATE: October
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                  LENGTH: 660 amino acids
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CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                        NUMBER: Provisional, see
October 28, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: S
US-09-458-791-8
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Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL EN
Query Match
Best Local Similarity
Matches 227; Conserv
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Best Local
                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION: -(Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COmpatible OPERATING SYSTEM: MS-DOS/Windows 95 SOFTWARE: Word for Windows 95, 7.0a
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                                                                                                                                                                                                                                                                                           NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/958,598 FILING DATE: 28-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
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                                                                                                                                                              LENGTH: 661 amino acids
                                                                                                                                                                                                                   TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
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   Conservative
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VIRAL ENCODED SEMAPHORIN PROTEIN
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                                                                                          SEQ
Score 1232; I
Pred. No. 7.2e
7; Mismatches
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Pred. No. 7.2e-96;
7; Mismatches 8;
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                                                                                          NO:
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             .2e-96;
                                  DB 4;
                                   Length 660;
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; MOLECULE TYPE:
US-09-459-066-8
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US-09-459-066-8
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                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Sprigg
                                                                                                                                                                               TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 8:
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ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Spriggs, Melanie TITLE OF INVENTION: VIRAL ENTITLE OF INVENTION: RECEPTOR
                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
                                                                                                                                                                                                                        NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS/Window SOTWARE: Word for Windows 95, CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                            TELEPHONE:
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                                                      Conservative
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                                                                                                                  protein
                                                                40.3%;
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                                                                                                                                                                                                                                                                                                        08/958,598
                                                  Score 1232; DB 4;
Pred. No. 7.2e-96;
"" wismatches 8;
                                                                            Length 660;
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                                                   Gaps
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                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043/
FILING DATE: 31-CAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: SG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SGARLATO, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: MEDLEN & CARROLL
f: 220 MONTGOMERY STREET,
SAN FRANCISCO
                                                                                        PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK--GGGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                               ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                 amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGS
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PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                             EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALIFORNIA
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                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGARLATO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC
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97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0,
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                                                                                                                                                                                                                                    Score 1225; DB : Pred. No. 6e-96;
                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30
                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                      4,
                                                                                                                                                                                                                                                 Length 232;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
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; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2
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                                                                                                          ; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-11
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US-09-180-100-11
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US-09-178-869-2
                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 360
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
                                   Query Match
Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09180100 Patent No. 6306395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tao, Weng
APPLICANT: Wong, Shou
APPLICANT: Hickey, William F
APPLICANT: Hammang, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/178,869B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225;
1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                     Conservative
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97.0%;
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97.0%;
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                                   Score 1225; D
Pred. No. 1.2e
3; Mismatches
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                                                  5; DB 4;
1.2e-95;
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                                   4;
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                                                                       Length 360;
                                   Indels
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                                   0,
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RESULT 8
US-08-236-311-7
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                                                                     US-08-236-311-7
Query Match
Best Local S
Matches 225
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                                                                                                                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/2
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                    FILING DATE: 02-OCT-1987 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/84 FILING DATE: 18-FEB-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9:
FILING DATE: 26-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
   Local Similarity
mes 225; Conser
                                                                                     LENGTH: 5/1
TYPE: amino acid
                                                                                                                                                                                                                                     NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: 5.25 inch, 360 Kb floppy disk
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                 40.0%;
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                                                                                                                                                                                                                                                    28,616
 Score 1225; D
Pred. No. 1.2e
3; Mismatches
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          1.2e-95;
   4
                                 Length 371;
   Indels
   0;
   Gaps
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1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

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NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT

120 199

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                                                 TOPOLOGY: US-08-457-918-7
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Patent No. 6117655
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                     NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
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                                                                                                             SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/1 PTILING DATE: 02-OCT-1987
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 28-SE
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 26-AU
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                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                 TYPE:
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r: 460 Point San Bruno Blvd
South San Francisco
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                 linear
                                                                                                                                                                             415/225-8228
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97.0%;
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   Score
Pred.
   1225; DB 3;
No. 1.2e-95;
                 Length 371;
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US-08-784-512-3
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                                                              GENERAL INFORMATION:
APPLICANT: BARTNIK
APPLICANT: EIDENMU
APPLICANT: BUETTNE
                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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LENGTH: 376
                                                                                                                            Sequence 3, Application US/08784512 Patent No. 5872209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAMURA, NO. 630
APPLICANT: NAGATA, Shigekazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: PCT EARLIER FILING DATE: 1997-05-01 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver.
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                                APPLICANT:
 TITLE OF INVENTION:
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                               BUETTNER, Frank
CATERSON, Bruce
HUGHES, Clare
                                                                                BARTNIK, Eckart
EIDENMUELLER, Bernd
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Pred. No. 1.2e-95;
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                        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 376
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US-08-784-512-3
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Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTORNEY/ACENT INFORMATION:
NUMBER: CERANDOS DATA: 196
                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
 APPLICANT: BARTNIK, Eckart
APPLICANT: EIDENNÜELLER, Bernd
APPLICANT: BUETTNER, Frank
APPLICANT: CATERSON, Bruce
APPLICANT: CATERSON, Bruce
TITLE OF INVENTION: and nattificial recombinant substrate (rAGG
TITLE OF INVENTION: and native aggrecan to study the proteolyt
TITLE'OF INVENTION: "Aggrecanase" in cell culture systems
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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Suite 500, 3000 K
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PCT-US95-03866-12
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                                                                                                                                       Sequence 12, Applicat GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acid
                                               APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
                NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 96100682.2 FILING DATE: 18-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                         Application PC/TUS9503866
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Suite 500, 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202)672-5300
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1..396
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Fish & Neave
                ADDRESS:
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Best Local S
Matches 225
                                                                                                                                                                                                                                                                     Sequence 14, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all stat.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO: 12:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                             APPLICANT: NOCKA, KATI (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
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TELEFAX: 212-596-9090
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NAME: Haley Jr, James F
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APPLICATION NUMBER: US 0
FILING DATE: 28-MAR-1994
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                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CytoMed/2
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                                                                                                     STREET: 1251 Avenue of the Americas CITY: New York
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                                                                     COUNTRY: United States of America
                                                                                                                                            ADDRESSEE:
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                                                                                          New York
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SYSTEM: PC-DOS/MS-DOS
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                  Floppy disk
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Pred. No. 1.5e-95;
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PCT-US96-10043-11
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    CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 60/
APPLICATION NUMBER: 14-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: Cy
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
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PRIOR APPLICATION DATA:
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                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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STREET: 2-
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                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                          COUNTRY: . USA
ZIP: 02210-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                           225 Franklin Street
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97.0%;
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                                            US 60/000,213
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Pred. No. 1.5e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 424;
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TELLERAX: 61//JZ.

TELLERAX: 61//JZ.

TELLEX: 200154

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENCTH: 437 amino acids
TYPE: amino acid
STRANDEDNEESS: not relevant
"OPOLOGY: linear
"OPOLOGY: linear
Search completed: July 15, 2003, 07:02:42 Job time: 23.8412 secs
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                                                                                                                                                                                                                                                                     Query Match 40.0%; Score 1225; DB 5; Length 437; Best Local Similarity 97.0%; Pred. No. 1.5e-95; Matches 225; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                      Gaps
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